Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	histidine-rich gly	histidine-rich gly			hypothetical prote	zinc finger protei	g,	knob-associated hi	hypothetical prote	cation efflux fami		cAMP response elem	hypothetical prote	zinc finger protei	MHC H-2K/t-w5-link	female-specific do	male-specific doub	zinc resistance pr	alpha-amylase homo	hypothetical prote	S59/2 homeotic pro	$\sigma$	hypothetical prote	probable membrane	d d	hypothetical prote	knob-associated Hi	hypothetical prote	probable histidine
SUMMARIES	āi	кснисн	A60488	KGZŐHL	A54523	T45059	T14155	T33997	A29454	H83994	F87286	178877	A45477	T23089	T30173	I49714	A32372	B32372	T27544	T39539	T48099	A36664	T43236	H82061	AD0262	AB3110	B98177	B71623	137	C64698
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	Query Match Length	1					1571								_								Н	242					-	
d	Query Match		52.1	25.0	22.5	20.0	18.2	18.0	17.8	17.7	17.3	17.2	17.2	17.2	17.2	16.8	16.6	16.6	16.4	16.1	16.0	15.5	15.5	15.4	15.2	15.2	15.2	15.1	15.1	15.0
	Score	996	503.5	241.5	217	193	176	173.5	171.5	170.5	167	166.5	166.5	166.5	166.5	162	9								147	4	4	ď.	ľ,	•
	Result No.	! !	7	ო	4	Ŋ	9	7	<b>6</b> 0	σι	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

histidine-rich cal	probable copper-tr	FB19 protein - hum	hypothetical prote	knob protein - mal	knob-associated hi	knob protein precu	histidine-rich pro	HRPII protein - ma	hypothetical prote	hypothetical prote	hypothetical prote	proline-rich prote	histidine/alanine-	extensin class I (	nodulin Enod2 - Se
434373	JC2464	JE0291	T30119	A26480	A54494	A54495	A28412	S31782	T28872	AC2680	A97462	S23737	A25942	S14983 .	S22140
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852 2 1	.,	7	102 2	270 2	473 2	634 2	634 2	301 2	997 2	905 2	916 2	297 2	309 2	130 2	330 2
14.9 852 2 7	731 1	940 2						14.7 301 2							
143.5 14.9 852 2 7	14.8 731 1 5	940 2	14.8	14.8	14.8		14.8	14.7	14.7	14.6	14.6	14.5	14.5	14.4	

# ALIGNMENTS

	RESULT 1 KGHUGH histidine-rich alveoprotein precursor - human
	Cipteries: now Septems (man) Cipter 4-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 16-Jun-2000 Cipterion: Noting: 02066
1	C.A.C.C.ESELOII: A012607, 223003 XXX.oide, 17
	Blochemistry 25, 220-2225, 1980 Aritle: Amino acid sequence of human histidine-rich glycoprotein derived from the nucle A.Deference number: An1287. MITD:86216149: PMID:3011081
	A;Acceston: A01287 A;Molecule type: mENA
	s: 1-525 <koi> eferences: GB:AB005803; NJ</koi>
	R:Hennis, B:; Haveldar, A:; Kluit, C. Submitted to the BMBL Data Library, October 1991 A. December on Dra Asterion of a dimendentide repeat in the human histidine-rich alycop
	Approximation of the control of the
	A;Status: preliminary
	A;Molecule type: DNA A;Residues: 214-247 <hen></hen>
	A;Cross-references: EMBL:Z17218; NID:g32453; PIDN:CAA78925.1; PID:g32454 C. Comment: Although its physiological function is not vet known. HRG does bind heme, dy:
	din, and the lysine-binding site of plasminogen. On the basis of its homology with HMW l
	lood coagulation cascade. C:Comment: The amino half of this protein is homologous to the first two cystatin-like (
	ould not have inhibitory activity.
	e-rich' region.
	C.Genetics:
	Ajdene: GDB:1RG A;Cross-references: GDB:120055; OMIM:142640
	A;Map position: 3q27-3q27
	C;Superraming: miscrannerical giycoprocenn, cystatan momercy; C;Keywords: duplication; glycoprotein; heparin binding; tandem repeat
	F;1-18/Domain: signal sequence #status predicted <sig> F:10-52k/Product: histidine-rich glycoprotein #status predicted <mat></mat></sig>
	F:19-131/Domain: cystatin homology <vi></vi>
	F;140-246,Domain: cystatin nomology <12.78-321/Region: proline-rich
	F,63,125,344,345/Binding site: carbohydrate (Asn) (covalent) #status predicted F,78-89,105-126,218-241/Disulfide bonds: #status predicted
	100.08;
	Best Local Similarity 100.0%; Pred. No. 8.88-75; Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 НРНКНЮЗНЕОНРИЭНИРИАНИРИЕНОТИКОНРИЭНИНРИСКИРИСКИРИСКИРИСКИРИСКИ 60

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Cispecies: Plasmodium lophurae
Cispecies: O. Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
R.Ravetch, J.V.; Feder, R.; Pavlovec, A.; Blobel, G.
Ricession: A2652, 1984
AyTitle: Primary structure and genomic organization of the histidine-rich protein of the AyEderence number: A22692; MUID:85061618; PMID:6095114
AyCossion: A22692
AyCossion: A22692
AyComment: There are two copies of 16-residue repeats, two copies of 17-residue repeats, Cigenetics:
A; Comment: There are two copies of 16-residue repeats, two copies of 17-residue repeats
Cigenetics:
A; Introns: 23/3
Cigenetics:
A; Introns: 23/3
Cigenetics:
A; Introns: 23/3
Cigenetics:
A; Introns: 21/3
Cigenetics:
A; Introns: 13/3
Cigenetics:
A; Introns: 14/5
Cigenetics:
A; Introns: 14
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histidine-rich protein - Plasmodium lophurae (fragment)
c;Species 13-oct-1994 #sequence_revision 15-oct-1994 #text_change 20-Aug-1999
C;Accession: A54523
R;Irving, D.O.; Cross, G.A.M.; Feder, R.; Wallach, M.
Mol. Biochem. Parasitol. 18, 223-234, 1986
A;Titte: Structure and organization of the histidine-rich protein gene of Plasmodium lop
A;Reference number: A54523; MUID:86174893; PMID:3007981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 РИННИНИНАРИНИНИНИРАРИНИННЯНАРИНИСТИВ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 РНКНЯЗНЕОНРИСНН-----РНАНИРИЕН-- ОТНКОНРИСНИРИСНИРИСНИРИС
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross.1-140 < IRV>
A;Cross-references: CBW15317; NID:g160331; PIDN:AAA29616.1; PID:g552196
C;Superfamily: plasmodium histidine-rich protein
C;Keywords: tandem repeat
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Pred. No. 9.4e-12;
2; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    РНКНИЯНЕДИРИСИНРИАНИРИЕНОТИRQИРИСИИРИСИИРИСИ - - -
                  histidine-rich glycoprotein precursor - Plasmodium lophurae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 241.5; DB 1;
Pred. No. 1.8e-13;
1; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
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Best Local Similarity 39.6%;
Matches 38; Conservative
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Best Local Similarity 47...
Best Local Similarity 47...
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B; Molecule type: momen.
Biophys. Res. Commun. 200, 78-82, 1994
A; Ralkier, T.; Andersen, H.; Vestergaard, A.; Magnusson, S.
Biochem. Biophys. Res. Commun. 200, 78-82, 1994
A; Ralte: Bovine histidine-rich glycoprotein is a substrate for bovine plasma factor XIII
A; Reference number: JC2196; MUID:94220160; PMID:7909439
A; Accession: JC2196
A; Molecule type: protein
A; Residues: 1-23;335-54, VW, 57-101, 'R'; TVGEXTEG', 116, 'N', 118, 'R', 120-136;137-145;150-26
A; Residues: 1-23;35-54, VW, 57-101, 'R'; Magnusson, S.; Halkier, T.
Tricmb. Res. 60, 385-396, 1990
A; Restergaard, A.B.; Andersen
B; Vestergaard, A.B.; Andersen
A; Molecule type: protein
C; Superfamily: histidine-rich glycoprotein; cystatin homology
C; Comment: This protein is a single-chained plasma protein which participates in transgl
C; Superfamily: histidine-rich glycoprotein; cystatin homology (fragments)
C; Superfamily: histidine-rich glycoprotein; plasma
F; 2-113/Domain: cystatin homology (fragments)
C; Superfamily: histidine-rich glycoprotein; plasma
F; 2-113/Domain: cystatin homology (fragments)
F; 122-207/Domain: cystatin homology (fragments)
F; 122-207/Domain: cystatin homology (fragments)
F; 124-24, 60-71, 80-108, 165-346, 180-203, 258-288/Disulfide bonds: #status experimental
F; 74,107, 164, 266/Binding site: carbohydrate (Asn) (covalent)
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Actions and a control of the distribution force.

Actions and a control of the distribution force.

Actions and a control of the distribution force.

C.Species: Bos primigenius taurus (cattle)
C.Species: Asconson, Cattle)
C.Species: Asconson and a control of the distribution of the 
                                                                                                                                                                                                 410 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 469
DFQDYGPCDPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 120
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; Pred. No. 1.3e-35;
15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                               LPLPEANFPSFPLPHHKHPLKPDNOPFP 148
                                                                                                                                                                                                                                                                                                                                                                      470 LPLPEANFPSFPLPHHKHPLKPDNOPFP 497
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hypothetical protein Y39B6B.gg [imported] - Caenorhabditis elegans

RESULT 3 KGZQHL

Fri Sep 24 09:03:21 2004

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hypothetical protein BH2760 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H83994
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir:
Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHHGHHHFPPF--WPPCPPPPFWPPHRRGGHCHHH 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.8%; Score 171.5; DB 2; Best Local Similarity 39.0%; Pred. No. 2.9e-07; Matches 32; Conservative 5; Mismatches 32;
            PIDQEMRSEEPHSE----ESHGDEP 1057
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            1037
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C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: 145659
R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, R;Wilson, R.; Ainscough, R.; Anderson, T.; Hillier, L.; Jier, M.; Johns B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; Stock, L.; Wilkinson-Sproat, J.; Wolldman, P.
A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. A;Reference number: S43531; MUID: 94150718; PMID: 7906398
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Roossion: 145659
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL-A132896; NID: 96434440; PIDN: CAB60938.1; PID: 96434473
A;Experimental source: Clone Y39B6B
A;Antrons: 18/1; 69/1
A;Note: Y39B6B.gg
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Cispeciaes Mus musculus (house mouse)
Cispeciaes: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
Ciscession: T14155
Ciscession: T14155
Ciscession: T14155
Rivarokua Y.; Kaneko-Ishino, T.; Kagitani, F.; Kohda, T.; Li, L.L.; Tada, M.; Suzuki, R. Rivarokua Genet. 12, 186-190, 1996
A;Title: Peg3 imprinted gene on proximal chromosome 7 encodes for a zinc finger protein. A;Reference number: Z17892; MUID:96154192; PMID:8563758
A;Reference T14155
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A,Residues: 1-1571 <KUR>
A,Cross-references: EMBL:AF038939; NID:g2791677; PID:g2791678; PIDN:AAB96922.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDYGPC------DPPPHNQGHCCHG-HGPPPGHLRRRGPG-------KGPRPFHC 103
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18.2%; Score 176; DB 2; Length 1571;
Best Local Similarity 36.5%; Pred. No. 2.7e-07;
Matches 31; Conservative 5; Mismatches 45; Indel8 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 193; DB 2; Length 73
Pred. No. 4.8e-09;
4; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 RQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKH 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 27.9%;
Matches 60; Conservative
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C;Keywords: zinc finger
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# Knob-associated histidine-rich protein precursor - malaria parasite (Plasmodium falcipa C, Species: Plasmodium falciparum C, Species: Plasmodium falciparum 2, Species: Plasmodium falciparum 2, Species: 3.1-Dec-1988 #text\_change 09-Jun-2000 C, Accession: A29454 R,Triglia, T.; Stahl, H.D.; Crewther, P.E.; Scanlon, D.; Brown, G.V.; Anders, R.F.; Kemj EMBO J. 6, 1413-1419, 1987 A,Title: The complete sequence of the gene for the knob-associated histidine-rich prote. A, Reference number: A29454; MUID:87275836; PMID:3301325 A,Accession: A29454 A,Residues: 1-657 <TRI>A,Residues: 1-657 <TRI>A,Cosse-references: GB:V00060; NID:g9908; PIDN:CAA68268.1; PID:g9909

Gaps

Indels 13;

Length 657;

57 AQKQHEHHHHHHHHHHQHQAPHQAPHQAHHHHHGEVNHQAPQVHQQVHGQDQAKHHHH 116

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||| |: : | | |
384 RNRAAATRCRQKRKVWVMSLEKKAEEL 410
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 48; Conserv
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Matches 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cation efflux family protein [imported] - Caulobacter crescentus
C.Species: Caulobacter crescentus
C.Species: Caulobacter crescentus
C.Species: Caulobacter crescentus
C.Accession: P87286
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; DeBoy, R.J.; DeBon, K.B.; Gwinn, M.L.; Haft, D.H.; Kolon
N. J.; Brmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A.Accession: F87286
A.Accession: F87386
A.Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Homo sapiens (man)
C.Species: L.Species: Homo sapiens (man)
C.Species: L.Species: L
                                                                                                                                                                                                                                                                A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06479.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2760
A,Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A,Reference number: A83650; MUID:20512582; PMID:11058132
A,Accession: H83994
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-380 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.7%; Score 170.5; DB 2; Length 380; 39.8%; Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.3%; Score 167; DB 2; Length 361; 50.0%; Pred. No. 4e-07; ive 3; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 ЕНСНЕЕООНИНННОЕОРНУМІОР 217
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Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 ;
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Best Local S
Matches 33
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F87286
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jun-2000
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jun-2000
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jun-2000
B;Nowura, N.; Zu, Y.L.; Maekawa, T.; Tabata, S.; Akiyama, T.; Ishii, S.
J. Biol. Chem. 268, 4259-4266, 1993
A;Title: Isolation and characterization of a novel member of the gene family encoding the A;Reference number: A45477; MUID:93179432; PMID:8440710
A;Recession: A45477
A;Residues: 1-508 «NOM»
A;Residues: 1-508 «NOM»
A;Residues: 1-508 «NOM»
A;Cross-references: GB:L05515; NID:g181049; PIDN:AA52072.1; PID:g181050
A;Cross-reference extracted from NCBI backbone (NCBIN:125837)
B;Zu, Y.L.; Maekawa, T.; Nomura, N.; Nakata, T.; Ishii, S.
A;Gene: CREBPA
C;Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding domain homol
F;231-271/Domain: fos/jun DNA-binding domain homology <FJD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding domain homol
F;370-410/Domain: fos/jun DNA-binding domain homology <FUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Zu, Y.L.; Maekawa, T.; Nomura, N.; Nakata, T.; Ishii, S.
Oncogene 8, 2749-2758, 1993
A;Title: Regulation of trans-activating capacity of CRE-BPa by phorbol ester tumor promc
A;Reference number: I58379; MUID:93390949; PMID:8378084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                     38 НРИОНОТЕРРИНРУРНОНОВАНИРИРОРИНООМИРИ-НИЅИЗИТИАНРАНИОТЅРИРРЕ 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 НРНОНОТСРРИНРУРНОНОНРАНИРНРОРННООМНРН-НИЅИЗИГНАНРАННОТЅРИРР 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---QPIGGRRRRVVDEDPDERRRKFLE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 HTGNQAQVSPATQQMQPTQTIQPP------QPTGGRRRRVVDEDPDERRRKFLE 244
                                                                                                                                                                                                                                                                                                 1 НРИКННЗ --- НЕОНРИСНИРИАНИРИВНОТИКО - ИРИСКИРИСИ - ИРИ- СИИРИСИНРИС
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 8-508 <2U11>
A,Cross-references: GB:L05911; NID:g181051; PIDN:AAC37525.1; PID:g181052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:9181056
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Local Similarity 32.7%; Pred. No. 6e-07;
les 48; Conservative 8; Mismatches 52; Indels 39
                                                                                                                                            Length 369;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 34-508 <ZUY2>
A; Cross-references: GB:L05913; NID:g181055; PIDN:AAC37526.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     H------HPHCHDFQDYGPCDPPHNQGHCCHGHGPPGHLRRR-
                                                                                                                                                DB 2;
                                                                                                                                                Score 166.5; DB 2;
Pred. No. 4.5e-07;
8; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cAMP response element-binding protein CRE-BPa - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: 178878
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 -----HCRQIGSVYRLPPLRKGEVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 RNRAAATRCROKRKVWVMSLEKKAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 HTGNQAQVSPATQQMQPTQTIQPP
                                                                                                                                                17.2%;
ilarity 32.7%;
Conservative
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A;Map position: 7p15-7p15
```

hypothetical protein H13N06.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T2-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000
C;Accession: T23089
R;Lennard, N
S;Meference number: Z19673
A;Reference number: Z19673
A;Reference number: Z19673
A;Accession: T23089
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-515 \*WIL>
A;Residues: 1-515 \*WIL>
A;Residues: 1-515 \*WIL>
A;Residues: 1-515 \*WIL>
A;Cross-references: EMBL: Z99942; PIDN: CAB17070.1; GSPDB:GN00028; CESP:H13N06.5
A;Experimental source: clone H13N06
C;Genetics:
A;Gene: CESP:H13N06.5
A;Map position: X
A;Introns: 118/1; 156/2; 182/2; 306/1

Length 515; Query Match
17.2%; Score 166.5; DB 2; Length
Best Local Similarity 28.5%; Pred. No. 6.1e-07;
Matches 39; Conservative 6; Mismatches 29; Indels 40 HHPHGH-----HPHGHHPHGHHPHCHDFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGP 94

-----НРИЕНОТИКОНРИСИИРИС 39

5 ННЅНЕОНРИСИНРНАН-----

ò g à g

95 GKGPRPFHCRQIGSVYR 111 à

:| |: -----SAKQVGDEYQ 195

Cipecies: Mus musculus (house mouse)
Cipecies: Mus musculus (house mouse)
Cipecies: Mus musculus (house mouse)
Cipate: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999
Cipate: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999
Cipate: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999
Cipate: 23.0754 Marazzi, G.; Yang, E.; Copeland, N.; Jenkins, N.; Spence, S.E.;
Dev. Biol. 177, 383-396, 1996
A;Title: Pwl, a novel zinc finger gene implicated in the myogenic and neuronal lineages.
A;Reference number: Z20754; MUID:96400442; PMID:8806818
A;Accession: T30173
A;Accession: T30173
A;Accession: T30173
A;Molecule type: DNA A;Residues: 1-1378 <REL>
A;Cross-references: EMBL:U48804; NID:gl197856; PID:gl197857; PIDN:AAC52770.1
A;Experimental source: strain Sv129; limb bud
C;Genetics:

, 2 Query Match 17.2%; Score 166.5; DB 2; Length 1378; Best Local Similarity 36.0%; Pred. No. 1.5e-06; Matches 31; Conservative 5; Mismatches 45; Indels 5;

2 РНКНИЅНЕОНРИGНИРНАНИРНЕН- DTHROНРИGНИРНGНИРНGНИРНGНИРНСН 60 ò g

61 DFQDYGPCDPPHNQGHCCHGHGPPP 86

ò

MHC H-2K/t-w5-linked ORF precursor - mouse (5/Species: Mus musculus (house mouse) (5/Species: Mus musculus (house mouse) (5/Accession: 149714 |
C)Accession: 149714 |
Mol. Cell. Biol. 10, 138-145, 1990 |
A/Title: A putative transmembrane protein with histidine-rich charge clusters encoded in A/Title: A putative transmembrane protein with histidine-rich charge clusters encoded in A/Accession: 149714; MUID:90097821; PMID:2294398 |
A/Status: preliminary; translated from GB/EMBL/DDBJ A/Status: preliminary; hanslated from GB/EMBL/DDBJ A/Status: 1436 <a href="https://doi.org/10.1007/NDBJ-1436">Molecule type: mRNA A/Residues: mRNA A/Residues: 1436 <a href="https://doi.org/10.1007/NDBJ-1436">Molecule type: mRNA A/Residues: m 43 HGHSHGHSHBDFHHGHSHGHSH----EDFHHGHCHTHESIWHGHAHSHBDHGHSREELH-H 97 1 НРИКИ-НЅНЕОНРИСИ-НРИАНИРИЕНОТИКОНРИСИ----ИРИСИ-НРИСИНРИСИНРИ Ouery Match 16.8%; Score 162; DB 2; Length 436; Best Local Similarity 42.9%; Pred. No. 1.3e-06; Matches 39; Conservative 2; Mismatches 32; Indels 98 GHSHGHSHDSLHHG----GHGHAHREHSHG 123 54 GH-HPHCHDFQDYGPCDPPPHNQGHCCHGHG 83 g 8

Search completed: September 23, 2004, 22:55:57 Job time : 31.7189 secs

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September 23, 2004, 21:23:24; Search time 101.044 Seconds (without alignments) 413.849 Million cell updates/sec
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966
1 HPHKHHSHEQHPHGHHPHAH......PSFPLPHHKHPLKPDNQPFP 148
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1: geneseqp1980s:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Abb79807 Rabbit h Abb79807 Rabbit h Abb79806 Human hi Adb76897 Human pi Adb79805 Rabbit h Abb79805 Rabbit h Abb7723 HRGP thm Abb72813 Novel hu Abg72531 Novel hu Abg72537 Novel hu Abg73535 Novel hu Abg73595 Novel hu Abg73599 Novel hu Abg73599 Novel hu Abg73599 Novel hu Abb7360 Peptide Abb3780 Peptide Abb3780 Peptide Abb3780 Peptide Abb3780 Puman bc Abb72108 Peptide Abb22108 Peptide Abb3780 Human li Aam06909 Human bc Abg52171 Human li Abg72171 Human li Abg72171 Human li Abg72171 Human li Abg7319 Human li Abg7319 Human li Abg7319 Human li
SUMMARIES	ABB79807 ABB79804 ABB79804 ABB79804 ABB79805 ABB07123 ABG27250 ABG27250 ABG27250 ABG27250 ABG27337 ABG23337 ABG235337 ABG23537 ABG23537 ABG23537 ABG23537 ABG23537 ABG23537 ABG23595 AAM18326 ABB37360 AAM18326 AAM18326 AAM08333 ABG22171 AAM05333 ABG40129 ABG40129
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Abg12879 Novel hum		Abb32509 Peptide #	Aam25978 Peptide #		Abbl8015 Protein #	Aam65721 Human bon		Abg47362 Human liv		Human		Novel		Abb67014 Drosophil	Abb71938 Drosophil	Aau74634 Oestrogen	Abg03494 Novel hum		Abb43409 Peptide #
ABG12879	AAM13580	ABB32509	AAM25978	ABB27363	ABB18015	AAM65721	AAM53343	ABG47362	AAM01333	ABG35350	ABG20509	ABG08412	AAU32905	ABB67014	ABB71938	AAU74634	ABG03494	AAM21094	ABB43409
124 4	82 4	82 4	82 4	82 4	82 4	82 4	82 4	82 4	82 4	82 5	324 4	304 4	79 4	372 4	449 4		266 4	156 4	156 4
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215	210	210	210	210	210	210	210	210	210	210	209.5	209	207.5	204.5	196.5	196.5	193	191.5	191.5
26	27	28	29	30	31	32	33	34	35	36	37	38	99	40	41	42	43	44	45

## ALIGNMENTS

ABB79807 ABB79807 ABB79807 ABB79807 ABB79807 ABB79807 ABB79807 AB707 AB7
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14-FEB-2002; 2002WO-US004336.

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cc multimer; a diagnostically useful HPRG-related composition, comprising the diagnostically labeled polypeptide, peptide or peptide multimer and a carrier; an antibody specific for an epptiope of HPRG that is present in the HFVP domain of human or rabbit HPRG, and which binds to HPRG or to any of the domain of human or rabbit HPRG, and which binds to HPRG or to any of the domain, or an antigen-binding fragment of the antibody; a method for the domain, or an antigen-binding fragment of the antibody; a method for that in the formation of the inhibiting cell invasion, cell proliferation or angiogenesis, a method for treating a subject having a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis; a method of detecting the presence of HPRG or its clavage product or its peptide in captural than or inhibiting angiogenesis in a subject; a method of detecting the presence of HPRG or its clavage product or its peptide in captural sample; isolated nucleic acids encoding the polypeptide, or peptide or peptide multimer; an expression vector; transformed or transfected cells; a method of providing to a cell, tissue or organ an angiogenesis-inhibitory amount of HPRG, an HFVP domain of HPRG or its pentabeptide, or the peptide multimer; an affinity ligand useful for binding to, or isolating, an HPRG-binding molecule, or isolating molecule, comprising the polypeptide, peptide or peptide compositions and methods are useful in diagnosing or tracting a disease or condition associated with undesired cell migration, invasion, for condition associated with undesired cell migration, invasion, or reating mantenes. HPRG-binding molecule, or isolating or erriching a disease or conditions and methods are useful in inhibiting the growth of primary temmours or metastases, and may also be used in treating neurodegenerative conditions or metastases, and any also be used in treating antibode or periode and any also be used in treating and endinged and and any also be used in tracery and an er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various
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100.0%; Pred. No. 4e-80;
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Best Local Similarity 100.
Matches 148; Conservative
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ABB79806 standard; protein; 148 AA. (first entry) 25-NOV-2002 ABB79806; RESULT 2 ABB79806 

22-AUG-2002.

cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian. Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; Human histidine proline rich glycoprotein His/Pro-rich domain. WO200264621-A2 Homo sapiens

The present sequence is the protein sequence of the histidine-prolinerich (HPP) domain of human anti-anglogenic histidine proline rich plycoprotein (HPRG see also ABB79804). Claimed anti-anglogenic plycoprotein (HPRG see also ABB79804). Claimed anti-anglogenic plycoprotein (HPRG see also ABB79804). Claimed anti-anglogenic and place of inhibiting anglogenesis, andothelial cell proliferation or endothelial cell and endotherally special or in vivo, or a pentagentically synthesised or recomplainally produced peptide multimers; a diagnostically labeled anti-anglogenic activity or the domains in a way which thinbits the anti-anglogenic activity of chromatom or habble composition, compraining cell adgression in antibody apported, peptide or peptide multimer and carrier; an antibody apported, peptide or peptide multimer and carrier; an antibody apported, peptide or the domains or rabbit HRRG-related composition, cort to any of the domains in a way which thinbits the anti-anglogenic activity of method for the domains or an antigen-binding fragment of the antibody; a method for inhibiting angieston, cell invasion, cell proliferation angiogenesis, or for inducing apoptosis; a method of carming the presence of HRRG or its cleavage product or itself or peptide multimer; an expression vector; transformed or transformed, or the poptide multimer; an expression vector; transformed or companies or isolating, an HRRG-binding onlecule, comprising the presence of HRRG or its of angiogenesis-inhibitory amount of HRRG and polypetide, peptide or peptide multimer; an expression vector; transformed or condition associated with undesired cell mignamethy inflammation, endometrically or carrier; and method of solating endometrically or carrier; and method of a solid suppor New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis. .; 0 stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various 100.0%; Score 966; DB 5; Length 148; 100.0%; Pred. No. 4e-80; ive 0; Mismatches 0; Indels Mazar AP; Plunkett ML, Claim 1; Page 13; 82pp; English. 14-FEB-2001; 2001US-0268370P. Conservative Donate F, Harris S, (ATTE-) ATTENUON LLC WPI; 2002-666989/71. Similarity P-PSDB; ABN84910. Sequence 148 AA; 148; Query Match Local Best Loca Matches 

ö 61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 120 61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 120 9 1 HPHXCHSHEQHPHGHHPHAHPHPHDHPHPHDTHRQHPHGHHPHGHHPHGHHPHGHHPHCH 1 НРНКНИЅНЕОНРИСНИРИАНИРИВНОТИКОНРИСНИРИСНИРИСКИРИСН Gaps

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The present sequence is the protein sequence of human histidine proline rich glycoprotein (HPRG), a proteinaceous metal chelator that can be used to inhibit anglogenais and treat cancer. Claimed anti-anglogenic polypeptides or peptides comprise: the histidine-proline-rich (H/P) domain (see ABB79806) of human HPRG; an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting anglogenesis, candothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808. Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or therapeutically labeled anti-anglogenic polypeptide, peptide or peptide multimer; a diagnostically useful HPRG-related composition, comprising the diagnostically labeled propeptide, peptide or peptide multimer; and antibody specific for an epitope of HPRG that is present in the H/P domain of human or rabbit HPRG, and which binds to HPRG or to any of the domains in a which inhibits the fartime and or articly of the domains in car an antigen-binding fragment of the antibody; a method for inhibiting or inhibiting condition associated with undesired cell migration, invasion, or anglogenesis, a method of stimulating or inhibiting anglogenesis, a method of detecting the presence of HPRG or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
                                                                                                                                                                                                                                                                                       Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; cytostatic; antiatarterioscelerctic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antialcer; osteopathic; antitumour; ophthalmological; noctropic; neuroprotective; antiparkinsonian; chelator.
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/note= "proline-rich domain"
/note= "Histidine-proline-rich domain, region also
specifically claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mazar AP;
                                                                                                                                                                                                                                                    Human histidine proline rich glycoprotein
                            121 LPLPEANFPSFPLPHHKHPLKPDNQPFP 148
LPLPEANFPSFPLPHHKHPLKPDNQPFP
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                                                                                                                                  ABB79804 standard; protein; 525
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its cleavage product or its peptide in a biological sample; isolated mucleic acids encoding the polypeptide, peptide or peptide multimer; an expression vector; transformed or transfected cells; a method of providing to a cell, tissue or organ an angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its pentapeptide, or the peptide multimer; an a faffinity ligand useful for binding to, or isolating, an HPRG-binding polypeptide, peptide or peptide multimer; immobilised to a solid support or carrier; and a method of isolating HPRG-binding molecule, or isolating or enriching cells expressing HPRG-binding site or receptor, from a complex mixture. The compositions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409
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                                                                                                                                                                                                                                                                                                                                                                                                invasion, proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers or fractures. HPRG is especially useful in inhibiting the growth of practures or meteatases, and may also be used in treating neurodegenerative diseases like Alzheimer's disease, parkinson's disease, and amyotrophic lateral sclerosis. The antibodies are stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 DPQDYGPCDPPPHNQGHCCHGHGPPPGHIRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV
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ive 0; Mismatches 0;
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nes 148; Conservative 0;
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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a CDNA. A protein encoded by the CDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the CDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid is sequence of a protein encoded by a CDNA differentially expressed in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ненкинѕивоненсингнаниенспитконенсингрисингисингненсинг
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/note= "Histidine-proline-rich domain, region also
specifically claimed in Claim 1"
treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8; Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 949; DB 8;
Pred. No. 5e-78;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Proline-rich domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPLPEANFPSFPLPHHKHPLKPDIQPFP 497
                                                                                                     Claim 1; SEQ ID NO 62; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.2%;
98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.6
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liver disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200264621-A2
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
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The present sequence is the protein sequence of rabbit histidine proline rich glycoprotein (HPRG), a proteinaceous chelator that can be used to inhibit angiogenesis and treat cancer. Claimed anti-angiogenic (H/P) polypeptides or peptides comprises the histidine-proline-rich (H/P) polypeptides or peptides changes the histidine-proline-rich (H/P) compained angiogenesis, and the profession or endothelial tube formation in vitro or a pertapeptide having the generic sequence given in ABBT9808.

Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or therapeutically labeled anigogenic polypeptide, peptide or peptide multimer; a diagnostically useful HFRG-related composition, comprising the diagnostically labeled or useful HFRG-related composition, comprising the diagnostically labeled or useful HFRG-related composition, comprising the diagnostically labeled or specific for an epicope of HFRG that is present in the H/P domain of specific for an epicope of HFRG that is present in the H/P domain of peptide than an entided or the domain, or an antiger-binding fragment of the antibody; a method for thibiting a method for inhibiting or an entider-binding fragment of the antibody; a method for inhibiting a condition associated with undesired cell migration, invasion, cell migration, cell migration, invasion, condition associated with undesired cell migration or angiogenesis, a method of stimulating the presence of HFRG or trelating a subject, a method of stimulating the presence of HFRG or trelating to a cell, tissue or organ an antiogenesis—inhibition and coding condition and method or transfected cells, a method of HFRG or the peptide or peptide multimer, immobilised to a sold support or carrier; and a method of isolating with un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invasion, proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative diseases like Alzhelmer's disease, parkinson's disease and amyotrophic lateral sclerosis. The antibodies are stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               890 HGHPPHGPPPHGHPPHGHPHGHGFHDHGPCDPPSHKEGPQDLH-QHAMGPPPKHPGKRGPGKGH 448
                                                                                                                                                                                                                                                New nistidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ззо Рисинрисррисинрисррисирриспродениров в рисиррисприст
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 РИКНИЅНЕОНРИСИНРИА-------НИ-----РИЕНDIНКОНРИСИНРИСИНР
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                                                                                                                           Mazar AP;
                                                                                                                           Plunkett ML,
                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 12-13; 82pp; English.
                        14-FEB-2001; 2001US-0268370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                           Harris S,
                                                                         (ATTE-) ATTENUON LLC
                                                                                                                                                                               WPI; 2002-666989/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 526 AA;
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14-FEB-2002; 2002WO-US004336.

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Thrombospondin; TSP-1; histidine-rich glycoprotein; HRGP, cytostatic; cardiovascular; protein therapy; gene therapy; antisense inhibition; ribozyme inhibition; antibody inhibition; angiogenesis; human; cancer;
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                                                                                                                                                                                                                                                                                                                                                                 HRGP thrombospondin (TSP)-binding domain fragment (residues 443-517),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombospondin-binding molecules and fragments comprising regions TSP-1 binding domains of Histidine-Rich Glycoproteins, useful for treating cancers and cardiovascular diseases.
                                449 FPFHWRIGSVYQLPPLQKGEVLPLPEANFPQLLLRNHTHPLKPEIQPFP
99 RPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQPFP
                                                                                                                                                                                                  Ş
                                                                                                                                                                                               ABB07123 standard; protein; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example, Fig 1, 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-DEC-2000; 2000US-00730379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Silverstein RL;
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SIMA/) SIMANTOV R. (SILV/) SILVERSTEIN R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-017220/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2001041670-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-1999;
                                                                                                                                                                                                                                                                                                           13-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2001
                                                                                                                                                                                                                                                     ABB07123;
                                                                                                                                                                 ABB0712
                                                                                                                                         RESULT
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The invention provides thrombospondin (TSP)-binding molecules and fragments comprising regions of the TSP-1 binding domains of Histidine-Richycoproteins (HRCP). The proteins are used for the regulation of cellular growth and proliferation, such as in the accretion of new blood vessels (angiogenesis), particularly for treatment of cardiovascular disease. They may be used for the reduction of angiogenesis, including growth suppression and arrest, and apoptosis in normal development, for example in embryogenesis, and in a wide range of disorders and diseases, including those involving tumours, malignancies, neoplastic and other pathological conditions and homeostatic imbalances in the control of growth and development, in particular anal cancer, bladder cancer, small call lung cancer, nor-small cell lung cancer, brace cancer, cancers cell adenosarcoma (DES), colorectal cancer, chondrosarcoma, class cancer, carvical cancer, chondrosarcoma, class cancer, carvical cancer, chondrosarcoma, class cancer, evenical cancer, chondrosarcoma, class cancer, leukemia, liver cancer, lumphoma, mesothelioma, oral cancer, voarian cancer, lumphoma, mesothelioma, oral cancer, ovarian cancer, stonach cancer, tryproid cancer, orangers cancer, skin cancer, squamous cell cancer, stonach cancer, testicular cancer, thyroid cancer, new cancer, lumpsarcoma, head and neck cancer and a cholangiocarcinoma. The present cancer represents the TSP-binding motif of HRGP
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Local Similarity
les 41; Conserv
Query Match
                       Best Loca
Matches
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                                                                                  0; Gaps
                                                                                                                    97 GPRPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                    Match 31.3%; Score 302; DB 5; Length 75; Local Similarity 100.0%; Pred. No. 4.1e-20; es 52; Conservative 0; Mismatches 0; Indels
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Sequence 75 AA;

Query Match

Best

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1;

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). (II) the polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity amino acid sequences of the invention. Note: The sequence data for this amino acid sequences of the invention. Note: The sequence data for this pleatent did not appear in the printed specification, but was obtained in electronic format directly from WHOO at 57 84 1 НРИКИНЅНЕОНРИСИНРИАНИРИЕНОТИКОНРИСИНРИСИИРИСИИРИСИНРИСИ New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. 3, Human, chromosome mapping, gene mapping, gene therapy, forensic food supplement, medical imaging, diagnostic, genetic disorder GPRPFHCRQIGSVYRLPPLRKGEVLPLPBANFPSFPLPHHKHPLKPDNQPFP DB 4; Length 245; 26.3%; Score 254.5; DB 4; llarity 48.2%; Pred. No. 2.8e-15; Conservative 2; Mismatches 39; Claim 20; SEQ ID NO 58378; 103pp; English. Novel human diagnostic protein #28010. ABG28019 standard; protein; 245 Tang YT; 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. (first entry) Drmanac RT, Liu C, WPI; 2001-639362/73. N-PSDB; AAS92206. (HYSE-) HYSEQ INC. Sequence 245 AA; WO200175067-A2. Homo sapiens 18-FEB-2002 11-OCT-2001 ABG28019; 25 셤 g

205 НРИНИНУНУНИННИНИНУНРУРНИЧНИНИНИНИНИНИНИНИНИНИНИНИН 264

Fri Sep 24 09:03:20 2004

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recation (PGR) primers, ollogomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) as useful in gene therapy techniques to restore normal cartivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of supplement. (II) and its binding partners are useful for treating disorders of supplement. (II) and its binding partners are useful for treating disorders of polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AgG00010-ABG30377 represent novel human diagnostic amino acid sequences. AgG00010-ABG30377 represent novel human diagnostic partent did not appear in the printed specification, but was obtained in electronic format directly from MPD at the printed specification, but was obtained in the printed specification but was obtained in the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant productions, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) is useful in gene therapy techniques to restore normal cartivity of (II) or to traat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and canno acid sequences. ABG00010-ABG30377 represent novel human diagnostic mainto acid sequences of the invention. Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the winter and produces.
                                        317
-----RGPGKGP 98
                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                      Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder.
    58 HCHDFQDYGPCDPPPHNQGHCCHGHGPPPGHLRR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 57609; 103pp; English.
                                                                                                                                                                                                                                                               Novel human diagnostic protein #27241.
                                                                                                                                              ABG27250 standard; protein; 406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                       ABG27250;
                                            265
                                                                                                      RESULT 9
                                                                                                                             ABG27250
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25.7%; Score 248.5; DB 4; Length 406; 32.6%; Pred. No. 1.6e-14; Indels 49; Gaps ive 3; Mismatches 41; Indels 49; Gaps

Query Match
Best Local Similarity 32.6'
Matches 45; Conservative

Sequence 406 AA;

233;

Length

25.1%; 35.0%;

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Sequence 233 AA;
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                                     265
                                                                                          290
           9
                                   61 DFQDYGPCDPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV
          1 НРИКИНЅИЕОНРИСИНРИАНИРИЕНОТИКОНРИСИИРИСИИРИСИИРИСИИРИСИИРИСИИРИСИ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wew isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                       Claim 20; SEQ ID NO 50126; 103pp; English.
                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #19758.
                                                                                                                                                                                                             ABG19767 standard; protein; 233 AA.
                                                                                                                  121 LPLPEANFPSFPLPHHKH 138
                                                                                                                                            294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631
                                                                                                                                             ----HHRH
                                                                                                                                                                                                                                                                  (first entry)
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N-PSDB; AAS83954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                   50 НИРИСИНРИСИВРОДУСРОВРРИNДСИССИСИСИСИСРРЕНТЯЯЯ СРОВЯВРИСЯ ОТОВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histidine-rich protein associated with plasmodium knob phenotype, and DNA encoding it - useful for in vitro diagnosis of P. falciparum infection.
                                                                                                                                                               52 НРИНИНИНКИЙНЕНИНИЦИЙНИННЕННЫ ТЯЗНУКНИЙНИНИНИКИНГИРИТИНИН 111
                                                                                                           49
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                                                                                                           ---HPHGHHPHG
                                                       Gaps
                                                 27;
                                                                                                        1 НРНКИНЅНЕО-НРНСИНРНАННРНЕН------БІНКОНРНСИНРНСН
                                                       Indels
                                                                                                                                                                                                                                                                                                                               110 YRLPPLRKGEV----LPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                                                                                                                                                                                                                                                                                                                                                                -AFGALEDSAVARTGLPLPEGVLCGAPTAAASAAVPPPAVPAP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malaria vaccine; Histidine-rich protein; cytoadherence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40. .42
/label= potential glycosylation site
Score 242.5; DB 4;
Pred. No. 3.2e-14;
3; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of Histidine-rich protein (HisRP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pro-peptide
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                                                       89
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/label= signal
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                                                       Conservative
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/label= 1
40. .42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-199590/24.
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                          Local Similarity
les 57; Conserv
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22-NOV-1992
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2000US-00649167.
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                                                                                                                                      Similarity 30.3 59; Conservative
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                                                                                                    Sequence 491 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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Best Local 9
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homologous DNA sequences in the P. lophurae genome. The sequence of mature proteins is arranged in numerous tandem repeats with up to mine histidine residues in a row, similar to other plasmodium proteins for which sequence data have so far been reported. (Updated on 25-MAR-2003)
                                                                                                                                                     РНКННЅНЕОНРНСНН-----РНАННРНЕН--- ОТНКОНРНСННРНСННРНСННРНС
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                                                                                                                              11;
                                                                                                     Length 351;
                                                                                                    Score 241.5; DB 2; Length
Pred. No. 6e-14;
1; Mismatches 34; Indels
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                                                                                                                                                                                                                                   267
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                                                                                                                                                                                                         HHPHCHDFQDYGPCDPPPHNQGHCCHGH
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                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #9940.
                                                                                                                                                                                                                                                                                                   ABG09949 standard; protein; 491
                                                                                                  25.0%;
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2000US-00649167
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Best Local Similarity
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N-PSDB; AAS74136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                    correct PD field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                              Sequence 351 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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(I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used
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responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the product of the product 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGHIRRRGPGKGP------RPF------HCRQIGSVYRLPPLRKGEVLPL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----HIPHGHHPHCHDFQ-DYGPCDPP------HNQGHCCHGHG-PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 SPPAHGHIQHHQHSGPYQHGHHQHRPPPAHGHHQHRSHHTAHHQ-HRSHQHGHHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 НСИНОНКРРРАНСИНОНСИНОНSSPPANCHИOHRHQPGHHQHRSPHSTAHHQHGHHQHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   НКННЅНЕОНР-НСНИРНЕ-----НОТНКОНРНСНИРН-----СНИРНСНИРНС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                   Claim 20; SEQ ID NO 55696; 103pp; English.
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genes. (I) is useful in gene thereby techniques to restore normal cartifuty of (II) or to treat dieease states involving (II). (II) iss useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this placetonic format directly from MIPO at electronic format directly from MIPO at the was obtained in the printed specification, but was obtained in the published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ненкинснерирненирналирненртиконридиненененирненирненирнен 60
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
in diagnostics as expressed sequence tags for identifying expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                            Length 183;
                                                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity 46.3%; Pred. No. 3.4e-13;
es 38; Conservative 1; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 53954; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #23586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG23595 standard; protein; 598 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DFQDYGPCDPPHNQGHCCHGH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                        Sequence 183 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
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ABG23595
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creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in degrostics as expressed sequence tags for identifying expressed control is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at the printed specification, but was obtained in electronic format directly from MIPO at (II). The printed specification, but was obtained in the printed specification, but was obtained in the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #4760 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 НРНКНЫЅНЕОНРНGН---НРНАНИРНЕНОТИКОНРНGH-НРНGНИРНGHИРНGHН
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 225.5; DB 4;
Pred. No. 2.9e-12;
4; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHCHDFQDYGPCDPPPHNQGHCCHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM18326 standard; protein; 292 AA
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26-WAY-2000; 2000US-0201456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.3%;
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 598 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM18326;
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CT The present invention relates to human single exon nucleic acid probes CC (SENP: see AAI10068-AAI20459). The present sequence is a peptide encoded CC (SENP: see AAI10068-AAI20459). The present sequence is a peptide encoded CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs C can be used to produce a single exon microarray, which can be used for CC measuring human gene expression in a sample derived from human cervical CC epithelial cells. By measuring gene expression, the probes are therefore UCC cervical cancer. Note: The sequence data for this patent did not form CC part of the printed specification, but was obtained in electronic format CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences SQ Sequence 292 AA;
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Search completed: September 23, 2004, 22:50:02 Job time : 105.044 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

0 ; Search time 17.2369 Seconds (without alignments) 447.085 Million cell updates/sec September 23, 2004, 21:27:50 Run on:

US-10-074-225A-5 966 1 HPHKHHSHEQHPHGHHPHAH......PSFPLPHHKHPLKPDNQPFP 148 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

S		Description		Q28640 oryctolagus		6							Q9pub8 brachydanio			8M6A60	013849	Q92504	Q48251	P16230	P13817	P09346	Q9wv48	P49907	P05227	Q9y566 ]	Q98sv1 brachydanio		F13983	Q45257 brad	008677 mus m	10571	P26410 rhodo	P55316 homo	# atim 700080
SUMMARIES		ID	HRG HUMAN	HRG RABIT	HRG BOVIN	HRPX PLALO	CSUP_DROME	KNOB PLAFN		KE4 MOUSE	DSX_DROME	AMY2 SCHPO	KE4 BRARE	FXB2 MOUSE	HMN1_DROME	PYGO DROME	CBPY_SCHPO	KE4 HUMAN	HPN HELPY	SRCH RABIT	KNOB PLAFA	KNOB PLAFG	SHK1_RAT	SELP BOVIN	HRP1 PLAFA	SHK1 HUMAN	SEPA BRARE	GSC DROME	EXTN TOBAC	HYPB BRAJA	KING MOUSE	MIN1 HUMAIN	HYPB RHOCA	FXGA HUMAN	TOTTOTAL TREE
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55 1 OTX1_RAT  99 1 NO75_SOVBN  71 1 SNVA_HAEIN  95 1 SRY MOUSE  63 1 SF01_MOUSE  12 1 EX24_ARATH  12 1 BRA2 DROWE  64 1 OTX1_HUWAN  72 1 YA1, HUWAN  72 1 SRY_MUSSP  1 SRY_MUSSP  1 NO75_PEA	Q63410 rattus norv P08297 glycine max P44526 haemophilus Q06738 mus musculu Q64213 mus musculu Q64213 mus musculu Q54256 drosophila P32242 homo sapien Q9upw0 homo sapien Q15637 homo sapien Q62663 mus spretus P16329 pisum sativ
23 25 25 27 27 27 27 27 27 27 27 27 27 27 27 27	OTX1 RAT NO75_SOYBN SNVA HAEIN SRY MOUSE SF0I_MOUSE BR42_ARATH BR42_BRATH CYX1_HUMAN YA1 HUMAN SF01_HUMAN SRY MUSSP NO75_PEA
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# ALIGNMENTS

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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Histidine-rich glycoprotein precursor (Histidine-proline rich
91lycoprotein) (HPRG) (Fragment).
                                                                                                                                                                                                                                                         ....', IPRO0010; Cystatin.
Pfam; PF00031; cystatin, 1.
SMART; SM00043; CY; 2.
Glycoprotein; Heparin-binding; Repeat; Signal; Polymorphism.
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 525;
                                                                                                                                                                                                                                                                                                                                                  HISTIDINE-RICH GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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A2B124D6CB93114F CRC64;
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    -!- SIMILARITY: Contains 2 cystatin-like domains.

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100.0%; Pred. No. 3.5e-70;
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CYSTATIN-LIKE 2.
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                                                                                                                                                       EMBL; M13149; AAA52694.1; -.
EMBL; AB005803; BAA21613.1; -
EMBL; Z17218; CAA78925.1; -.
                                                                                                                                                                                                    PIR; A01287; KGHUGH.
SWISS-2DPAGE; P04196; HUMAN.
Genew; HGNC:5181; HRG.
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                                                                                                                                                                                                                                                                                                                                                  63
87
125
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204
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                             coagulation cascade.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
DOMAIN: In addition to having a high His and Pro content, this protein has many internal repeats. 15 tandem repetitions of a 5-
residue sequence (G[H/P][H/P]PH, consensus) form a His/Pro-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----- РИЕНОТИКОНРИСИИРИСИИР
                                                                                                                                         glycoprotein.";
Biochmeistry 35:1925-1934(1996).
-!- FUNCIION: The physiological function is not yet known. It binds heme, dyes and divalent metal ions. It can inhibit rosette formation and is known to interact with heparin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HWW kninogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
SEQUENCE FROM N.A., AND SEQUENCE OF 9-23; 301-313 AND 422-429
                                                  MEDINE-9622917; PubMed-8639676;
Borza D.-B., Tatum F.M., Morgan W.T.;
"Domain structure and conformation of histidine-proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.2%; Score 543; DB 1; Length 526; Best Local Similarity 57.6%; Pred. No. 1.6e-36; Matches 98; Conservative 8; Mismatches 40; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HISTIDINE-RICH GLYCOPROTEIN.
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(BY PLASMIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSTATIN-LIKE 1. CYSTATIN-LIKE 2.
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InterPro, IPR00010; Cystatin.
Pfam; PF00031; cystatin; 1.
SMART; SM00043; CY; 2.
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**REDUINE=93351678; PubMed=8348977;

**MEDLINE=93351678; PubMed=8348977;

**REDUINE=93351678; PubMed=8348977;

**REDUINE=93351678; PubMed=8348977;

**Determination of the disulphide bridge arrangement of bovine histidine—rich glycoprotein...;

**FEBS Lett. 328:286-290(1993).**

**L. FUNCTION: The physiological function is not yet known. It binds heme, dyes and divablent metal ions. It can inhibit rosette formation and is known to interact with heparin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HWW Kininogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood coagulation cascade.

**CORTION'S Secreted bight His and Secreted in plasma.**

**CORTION'S Secreted bight His and Pro content, this protein has many internal repeats. 12 tandem repetitions of a 5-residue sequence (GHHPH, consensus) form a histidine-rich region.

**CORTION'S CORTION'S CORTION'S CORTION'S PORTION'S POR
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                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                           HRG BOVIN STANDARD; PRT; 396 AA.
33433;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
HISTARA-2004 (Rel. 43, Last annotation update)
HISTIGINE-rich glycoprotein (Histidine-rich glycoprotein)
(HPRG) (Fragments).
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; 128A8223499DE6FC CRC64;
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CYSTATIN-LIKE 2.
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                                                                                                                                                                                                                                                                                                                                    Bovidae, Bovinae, Bos.
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396 AA;
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Best Local Similarity
Matches 88; Conser
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RESULT 3
HRG_BOVIN
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                                     PPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDN 144
                                                          54
259 HSSDE----HHPHGHHPHGHHPHGHHPHGHHPPDNDFYDHGPCDPPPHR------P 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 РНКНИЅНЕОНРИСИН-----РНАИНРИЕН--ОТИКОНРИСИНРИСИИРИСИНРИСИНРИС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANBOUS: In the intraerythrocytic stages of development of P. Pophurae in ducks, there is a synthesis of a major protein that accumulates to comprise at least 50% of the cellular mass: the histidine rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ravetch J.V., Feder R., Pavlovec A., Blobel G.; "Primary structure and genomic organization of the histidine-rich protein of the malaria parasite Plasmodium lophurae."; Nature 312:616-620(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HISTIDINE-RICH GLYCOPROTEIN.
N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 241.5; DB 1; Length
Pred. No. 1.1e-12;
1; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-2.
18 X 10 AA TANDEM REPEATS.
D19A48D47D890453 CRC64;
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2 X 16 AA TANDEM REPEATS.
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2 X 17 AA TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                         351 AA.
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                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Last sequence upd
15-JUL-1999 (Rel. 38, Last annotation v
Histidine-rich glycoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=85061618; PubMed=6095114;
                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44032 MW;
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                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             Plasmodium lophurae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
139
173
351 AA;
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ses 42; Conser
                                                                                                                    145 OPFP 148
                                                                                                                                                           QAFP 368
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P04929;
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SEQUENCE
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HRPX_PLALO
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RAGINELNE-20186006; Pubmed=10731132;

RAGINELNE-20186006; Pubmed=10731132;

RA Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Galle R.P., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutron G.C., Worter E.G., Holt E.W., Nabhurner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.C., Wogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Addon R.M., Davie C., Baldwin D., Ballow R.M., Basus A., Barandala B.C., Champe M., Pfeiffer B.D., RA Ballow R.M. Basus A., Barandala B.P., Bhandari D., Bolshakov S., Ballow R.M., Basus A., Barandala B.P., Bhandari D., Bolshakov S., Rosenson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ballow R.M., Cawley S., Dallker G., Davenport L.B., Davies P.M., Cadarel J.M., Cawley S., Dallker C., Davenport L.B., Davies P.M., Davier M., Cabriella B., Delcher A., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Boutin R.J., Evangelista C.C., Ferraz C., Ferrisa C., Ferrisa C., Ferrisa C., Ferrisa C., Ferrisa C., Ferrisa C., Jalai M., Kalush F., Karpen G.H., Galbart W.M., Glasser M., Houston K.A., Mattei B., McInton G.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ling Y., Mattei B., McInton K.A., Mixon K., Moried M.P., McIeson D.L., Northe S.M., Moy M. Wurphy B., Murphy L., Muzny D.M., Nelson D.L., Abeller D. R., North K.A., Nixon K., Nusskern D.R., Pacheler J., Shan R., Shiera S., Wang Z.-Y., Wassarman D.A., Wainson W., Stupskin M.P., Shier B., Syriekas R., Tector C., Turner E., Vann S., Zhu X., Smith H.O., Albeng Z.-Y., Wassarman D.A., Weinsten B., Shier E., Spradling A.C., Stapleton M., Stupskin M.P., Shord J., Shu M., Shord K., Shun B., Syler B., Shriekas R., Mang Z.-Y., Wassarman D.A., Weinster B., Shu Wang Z.-Y., Wassarman D.A., Weinster B., Shu Wang Z.-Y., Wassarman D.A., Weinster B., Shu Wang Z.-Y., Wassarman D.A., Wein H. Wang Z.-Y., Warsarman D.A., Wein H. W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley; TISSUB=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
Garlson J.W., Erommiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
                                                                                                                                                                                                                                                                          Stathakis D.G., Burton D.Y., McIvor W.E., Krishnakumar S., Wright T.R., O'Donnall J.M.; "The catecholamines up (Catsup) protein of Drosophila melanogaster functions as a negative regulator of tyrosine hydroxylase activity.";
                                                                                                                                               Drosophia melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
CATSUP OR CG10449.
                                            449 AA
                                                                                                                                                                                                                                                             MEDLINE=99403013; PubMed=10471719;
                                                                                                                                                                                                                                                                                                                                     Genetics 153:361-382(1999)
                                          STANDARD;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 KPDLDMSTIWLHSIGSTLLISAAPFVLLYIIPLDNSEAMKPRLKVLLAFASGGLLGDAFL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 НІГРНАТНРНЅНОЕНСНОНОНОНОННЯНН-- ОСВЕНЕНСН- SHDMSIGLWVLGGIIAFLSVE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
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-!- FUNCTION: KAHRP might mimick human histidine-rich glycoproteins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 НКННЅНЕО́НРНСННРНАННРНЕНБТНКО́НРНСННРНСН-----НРНСННРНСН-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase, FBgn0002022, Catsup.

Ogy, GO:00000300, P:nurse cell/Occyte transport (sensu Insecta); IMP.
InterPro, IPR003689, Zn_transpt_Zip.

Pfam, PF02535, Zip, 1.
                       FUNCTION: Negatively regulates tyrosine hydroxylase activity. SUBSCELLULAR LOCATION: Integral membrane protein (Probable). SIMILARITY: Belongs to the ZIP transporter (TC 2.A.5) family. KE4/Catsup subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINKED (GLCNAC. . .) (POTENTIAL) F7111A254C07AB4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 196.5; DB 1; Length 449;
Pred. No. 5.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate NF7 / Ghana).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=5842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HPHGH-----HPHCHDFQDYGPCDPPHNQGHCCH----
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GHGPPPGHLRRRGPGKGPRPFHCRQIGS 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48658 MW;
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395
316
449 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fransport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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CARBOHYD
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                                                                                                                                                                                                                                                                                                     2
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    57 АДКДНЕННИННИННИННОВОДАРИДАРИДАННИНИНСЕУЛИДАРДУИДДУИЗОДДЕНИНИ 116
                                                                                                                                                                                                                                                                                                                           anchor host thrombospondin or a parasite analog in a binding complex with the endothelial cell receptor. SUBCELLULAR LOCATION: Cytoplasmic side of the membrane of infected
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                    POTENTIAL.
KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN.
HIS-RICH.
N-LINKED (GLCNAC. . .) (POTENTIAL).
F6991B9CCF98F946 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lennard N.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUMAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the ZIP transporter (TC 2.A.5) family.
                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z99942; CAB1700.1; -.
PIN; T23089; T23089; T23089; T23089; T23089; T23089; Zip.
InterPro; IPR003689; Zn_transpt_Zip.
Pfam; PF02535; Zip; 1. Transport; Transmembrane; Glycoprotein.
Hypothetical protein; Transport; Transmembrane; Glycoprotein.
TRANSMEM 27 69 POTENTIAL.
                                                                                                                                                                                                                                                                             Length 657;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical Ke4-like protein H13N06.5 in chromosome X. H13N06.5.
                                                                                                                                                                                                                                                                          Score 171.5; DB 1;
Pred. No. 7.4e-07;
5; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515 AA
                                                                                                                                                                                                                                                                                                                                                                                                    117 HHHHLHPQQPQGTVANPPSNE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                54 GHHPHCHDFQDYGPCDPPHNQ 75
                                                                                                                                                                                                       1 34 POTI
35 657 KNOI
61 123 HTS
42 42 N-L.
657 AA; 71941 MW; FV
                                                                                                                                                                                                                                                                             17.8%;
                                                                                                                                                                  EMBL; Y00060; CAA68268.1; -. PIR; A29454; A29454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KE4/Catsup subfamily.
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 39.0
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                           Malaria; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                            erythrocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 ННОСНОНАНОСНОНАНОАОСССРУАКААААЕААТАААНОНСНАНОНОНСНАНОНС-НАНО 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 HHPHGH-----HPHGHHPHGHHPHCHDFQDYGPCDPPHNQGHCCHGHGPPPGHLRRRGP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .-----НРНЕНОТНКОНРИСИНРИС 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
MEDILINE=90097821; PubMed=2294398;
St Jacques B., Han T.-H., Macmurray A., Shin H.-S.;
"A putative transmembrane protein with histidine-rich charge clusters encoded in the H-2K/tw5 region of mice.";
Moi. Cell. Biol. 10:138-145(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jubmitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
Jubmitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
Jubmitted SUBCELLUIAR LOCATION: Integral membrane protein (Probable).
Jubmitted SPECIFFICITY: Expressed abundantly in embryonic carcinoma cells, but weakly in adult tissues.
Jubmitted States and States and States and States (TC 2.A.5) family.
KE4/Catsup subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L., Hall J., Lasky S., Hood L., "Sequence of the mouse major histocomaptibility locus class II
                                                                                                                                                               (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                 .5; DB 1; Length 515;
1.5e-06;
thes 29; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KE4 MOUSE STANDARD; PRT; 476 AA.
031125, 0921W1;
031125, 0921W1;
031125, 0921W1;
16-OCT-2001 (Rel. 45, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2104 (Rel. 43, Last annotation update)
15-MAR-2104 (Rel. 43, Last annotation update)
16-MISTIGINE-rich membrane protein Ke4).
SLC39A7 OR HKE4 OR H2-KE4.
                                                                                                                                                                                                                                                                  LINKED (GLCNAC. . .) (PC 17D7E854F4E1DAAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 ннанзноввернина-нанонизн--врид----
                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Score 166.5;
                                                                        POTENTIAL.
POTENTIAL.
HIS-RICH.
N-LINKED (G
N-LINKED (G
N-LINKED (G
                       POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                    .
Ю
                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 GKGPRPFHCRQIGSVYR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SAKÖVGDEYQ 195
                                                                                                                                                                                                                                                                                                     55500 MW;
                                                                                                                                                                                                                                                                                                                                                    17.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ННЅНЕОНРИСИНРИАН-
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 28.5
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                        488
515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
STRAIN=129/SvJ;
214
2294
2294
423
203
7
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EMBL; M25292; AAA17840.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION
    1 НРИКН-НЅНЕОНРИСН-НРИАНИРНЕНБТИКОНРИСН----ИРИСН-НРИСНИРИСНИРИ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 HGHSHGHSHEDFHHCHSHGHSH----EDFHHGHGHTHESIWHGHAHSHDHGHSREBLH-H 97
                                                                                                                                                                                                                                                                                                   V -> L (IN REF. 1).
ACALLTEGGAVDSDVAGGAGPGWVLPFTAGGFIYVATVSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Larva, and Pupae;
MEDLINE=89168431; PubMed=2493994;
Burtis K.C.',
Bartis K.C.',
"Drosophila doublesex gene controls somatic sexual differentiation by producing alternatively spliced mRNAs encoding related sex-specific polypeptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20196006; PubMed=10731132;
MEDLINE-20196006; PubMed=10731132;
MEDLINE-20196006; PubMed=10731132;
Mannatides P.G., Scherer S.E., Holt R.A., Foskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                            PELLREASPLOSILEVLGILGGVAMMYLIAHLE -> RV
SPREGGWTVTWQVVQVLAGSCHSLQADLST (IN REF.
                                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Moptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                          16.8%; Score 162; DB 1; Length 476; 42.9%; Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     48214438BE44919B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS FEMALE AND MALE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHSHGHSHDSLHHG-----GHGHAHREHSHG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GH-НРИСНОРОДУСРСОРРРИМОСИСИБИБ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                           HIS-RICH.
N-LINKED (
                                                                                               Transmembrane; Glycoprotein
                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                          HIS-RICH.
                 EMBL; AF100956; AAC69903.1; -.
MGJ; MGI:5909; H2-Ke4.
InterPro; IPR003689; Zn_transpt_Zip.
Pfam; PF02535; Zip; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM MALE).
                                                                                                                                                                                                                                                                                                                                                                                                   476 AA; 50656 MW;
EMBL; M32010; AAA37767.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56:997-1010(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Doublesex protein.
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                                                                                           Transport; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DROME
                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                          TRANSMEM
                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIS-RICH.
SER/GLY-RICH.
ARVEINRTVAQIYYNYYTPWALVNGAPMYL -> GQYVVNE
YSRQHNLNIYDGGELRNTTRQCG (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 АНАННУНМААААААSVAQHQHQSHPHSHHHHHQNHHQHPHQ------QPATQTALRSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         РИСИНРИ------СИНРИСИНРИСИРИ--СИНРИСИРГОДУСРСОР-----РР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMYZ_SCHPO STANDARD; PRT; 774 AA.
042918; Q96WR2;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable alpha-amylase meu7 precursor (EC 3.2.1.1) (1,4-alpha-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS40000; DM_DOMAIN_1; 1.
PROSITE; PS50809; DM_DOMAIN_2; 1.
Sexual differentiation; Alternative splicing; DNA-binding;
Transcription regulation; Nuclear protein; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Female).

Missing (in isoform Female).

/FTId=VSP 001321.

/FTId=VSP 001322.

->A,H ABOLISHES DNA-BINDING.
H->Y: ABOLISHES DNA-BINDING.
H->Y: ABOLISHES DNA-BINDING.
C->Y: ABOLISHES DNA-BINDING.
C->Y: ABOLISHES DNA-BINDING.
C->Y: ABOLISHES DNA-BINDING.
R->Q: ABOLISHES DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.6%; Score 160; DB 1; Length 549; 28.8%; Pred. No. 5.2e-06; ive 3; Mismatches 37; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3C1B92724E4CE083 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 НРНКННЅНЕОНРНСНИРНАНИРИЕ-ИОТИКО-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSD-----HGGSVGPATSSSGGGAP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNQGHCCHGHGPPGHLRRRGPGKGP 98
EMBL; M25293; AAA17841.1; -.
EMBL; M2524; AAA17842.1; -.
EMBL; AZ003676; AAF54168.1; -.
PIR; A32372; A32372.
PIR; B32372; B32372.
PDB; ILPV; O2-OCT-02.
TRANSPAC; T00955; -.
FLYBASE, FBGN0000504; dsx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57409 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
224
296
427
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50
59
68
70
91
549 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3D-structure.
DNA_BIND 1:
DOMAIN 1:
DOMAIN 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
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MUTAGEN
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AMY2_SCHPO
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                                                                                                                                                                                                                                                                             RK SETAIN=9'19', Welliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RADLINE=21848401; PubMed=11859360; RA MODOJ V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Rajandream M.A., Lyne M., Lyne B., Bowan S., Roguros J., Peat N., Hayles J., Basham D., Bowan S., Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks R., Goble A., Hamlin N., Harris D., Hidago J., Hodgson G., Ra Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Moules L., Jones M., Leather S., McDonald S., McLean J., RA Holroyd S., Moules M., Sarason D., Quail M.A., Rabbinowitsch E., RA Collver K., O'Neil S., Mungall K., Murphy L., Niblett D., Odell C., RA Rollon S., Simmonds M., Squares B., Seeger K., Sharp S., RA Stevens K., Stevens K.
glucan glucanohydrolase) (Meiotic expression upregulated protein 7).
MEU7 OR SPBC16A3.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CD16-1;
MEDLINE=21270454; PubMed=11376151;
MEDLINE=21270454; PubMed=11376151;
Matanabe T., Miyashita K., Saito T.T., Yoneki T., Kakihara Y.,
Nabeshima K., Kishi Y.A., Shimoda C., Nojima H.;
"Comprehensive isolation of meiosis-specific genes identifies novel proteins and unusual non-coding transcripts in Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 29:2327-2337(2001).

-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CATACTOR In Oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 1 calcium ion per subunit (Potential).
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GeneDB SPombe; SPBG16A3.13; --
InterPro, IPR006047; Alpha_amyl_cat.
Pfam; PF0012B; alpha-amylase; II
Meiosis; Carbohydrate metabolism; Hydrolase; Glycosidase;
Calcium-binding; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE ALPHA-AMYLASE MEU7.
BY SIMILARITY.
BY SIMILARITY.
                                                                            Schizosaccharomyces pombe (Fission yeast).
Enkaryota, Pungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL021748; CAA16864.1; -. EMBL; AB054318; BAB60884.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 525-774 FROM N.A.
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553
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HSSP; P56271; 2AAA.
                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 HKPWKHEEHCSCHHDKPPRPVPHNGTKPDHKPWKHEEHCHHGKFPRPIPHNGTKPDHKPW 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 KHEEHCHHGRFPRPVPHNGTKPDHKPWKHEEHCSCHHDKFS-----RPVPHNGTKPDHKP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKHHSHEQHPHGHH-----PH----AHHPHEHDTHRQH-----PHG----HHPH 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 WKHEEHCHHGKFLRPUPHNVTKPDHKPWKHEEHCH-------HGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---QGHCCHGH--GPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEVLPLPEANFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GННРИСНН------РНG-----ННРИСННРИС---НD-FQDYGPCDPPRIN-----
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15-MAR-2004 (Rel. 43, Last annotation update)
Zinc transporter SLC39A7 homolog (Histidine-rich membrane protein Ke4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murray B.W., Stelltmann H., Klein J.;
Murray B.W., Stelltmann H., Klein J.;
"Identification of a homolog of the human HKE4 gene in zebrafish.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ datebases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the ZIP transporter (TC 2.A.5) family.
KE4/Catsup subfamily.
                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.1%; Score 155.5; DB 1; Length 774; 26.8%; Pred. No. 1.6e-05; ive 12; Mismatches 52; Indels 81.
                                       (VIA CARBONYL OXYGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89459 MW; 92CEAAE45664269B CRC64;
CALCIUM 1 (POTENTIAL)
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(POTENTIAL).
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16-OCT-2001 (Rel. 40, Last seq.
15-MAR-2004 (Rel. 43, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 26.8
les 53; Conservative
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CARBOHYD
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                                                                                                              DISULFID
                                                                                                                                                                                                                             DISULPID
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KE4_BRARE
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EMBL; AF196345; AAF05821.1; -.

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                                                                                                                                                                                                                                                                         44
                                                                                                                                                                                                                                                                                                  24 НЅННННGHGDGGCHGHSHGGAKMHHGASKWSAEANLPHAEEEHHVHDHGHTHDHA-HDHG 82
                                                                                                                                                                                                                                                                       1 НРИКИНЗИ----ЕОНРИС----НН-----РНАНИРИЕНОТИКОНРИСИ-ИРИСИНРИС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-97014266; PubMed=8861101;
Kaestner K.H., Schuetz G., Monaghan A.P.;
"Expression of the winged helix genes fkh-4 and fkh-5 defines domains in the central nervous system.";
min the central nervous system.";
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93361500; PubMed=7689224;
Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H.,
Monaghan A.P., Schuetz G.;
"Six members of the mouse forkhead gene family are developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1.1.
                                                                                                                                         HIS-RICH. (POTENTIAL).
                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                               DB 1; Length 352;
                                                                                                                                                                                                              Score 154; DB 1; Length 35
Pred. No. 1e-05;
2; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLUTAR LOCATION: Nuclear.
-1- DEVELOPMENTAL STAGE: Expressed during embryogenesis.
-1- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                    CBC8C60F6D2BA8A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-NOV-1997 (Rel. 39, Last annotation update)
FOYKhead box protein B2 (Transcription factor FKH-4).
FOXE2 OR FKH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulated.",
Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                428 AA
                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                               POTENTIAL.
POTENTIAL.
HIS-RICH.
                                          Transmembrane; Glycoprotein
               InterPro; IPR003689; Zn_transpt_Zip.
Pfam; PF02535; Zip; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                              45 Н-НРИСИ- НРИСИ 61
                                                                                                                                                                                  37922 MW;
ZFIN; ZDB-GENE-991110-20; ke4
                                                                                                                                                                                                                 15.9%;
                                                                                                                                                                                                                             L Similarity 42.7%;
35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                    148
181
235
105
217
311
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HSSP; Q63245; 2HFH.
                                                                    128
161
215
218
24
177
311
352 AA;
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Q64733;
                                           Transport;
                                                                                                                                         DOMAIN
CARBOHYD
NON TER
SEQÜENCE
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DOMAIN
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FXB2 MOUSE
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PIR; A36664; A36664.
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TRANSFAC; T04257;
    10;
                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley;
MEDLINE=2018606; PubMed=10731132;
MEDLINE=2018606; PubMed=10731132;
Amanatides P.G., Scherer S.E., Inl P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelfer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendalle J., Bayraktaroglu L., Beasley B.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91099659; PubMed=1980118;
Dohrmann C., Azpiazu N., Frasch M.;
"A new Drosophila homeo box gene is expressed in mesodermal precursor cells of distinct muscles during embryogenesis.";
Genes Dev. 4:2098-2111(1990).
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                                                                                                                                                                                                                                                                                                                              59 CHDFQDYGPCDPPPH--NQGHCCHGHGPPPGHLRRRGPGKGPRP-------
                                                                                                                                                                                                                                                                                                                                                     ----PQPPPPPPPPPHWVPYFHQQPAPAPQPPHLPSQ-PAQQPQPQSQPPQTSHPGKMQEA
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HANI_DROME STANDARD; PRT; 659 AA.
P22867; Q9VD96;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Homeobox protein slou (S59/2) (Slouch protein) (Homeobox protein NK-
                                                                                                                                                                                                                                                                                                                                                                                                218 AAVAAAAAAAAAVGSVGRLSQFPPYGLGSAAAAAAAAAA --TTGFKHPFAIEN
                                                                                                                                                                                                                                                                                                                                                                         -----FHCRQIGSVYRL---PPLRKGEVLPLPEANFPSFPLPHKHPLKPDN
                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                     Score 154; DB 1; Length 428;
Pred. No. 1.2e-05;
6; Mismatches 66; Indels
                                          PRINTS; PRO0053; FORKHEAD.

PRODOM; PD000425; TF Fork_head; 1.

SMART; SM00339; FH; 1.

PROSITE; PS00657; FORK HEAD 1; 1.

PROSITE; PS00658; FORK HEAD 2; 1.

PROSITE; PS00039; FORK HEAD 3; 1.

DNA-binding; Nuclear protein; Transcription regulation.

DNA_BIND 12 103
                                                                                                                                                                                                      POLY-ALA.
DB8A8EFD1E94AB10 CRC64;
                                                                                                                            FORK-HEAD.
POLY-HIS.
                                                                                                                                              POLY-HIS.
POLY-PRO.
POLY-ALA.
                                                                                                                                                                               POLY-ALA.
POLY-ALA.
                         Fork_head
                                                                                                                                                                                                                45170 MW;
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                                                                                                                                                                                                                                      15.9%;
29.5%;
TRANSFAC; T02442; -. MGD; MGL:1347468; Foxb2. InterPro; IPR001766; TF Ft Pfam; PF00250; Fork_head;
                                                                                                                                                                                                                                                              52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLOU OR NK1 OR $59 OR
                                                                                                                                                                              249
321
396
428 AA;
                                                                                                                                                                                                                                                  Local Similarity
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SEQUENCE
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Matches
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EMBL; AF457206; AAL91369.1; -. EMBL; AY075095; AAL79357.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
   257
                                                                                                                                                                                                                                                                                            229
                                                                                                                                                                                                                                                                                                              63 QDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEVLP 122
                                                                                                                                                                                                                                                                        62
FlyBase; FBGN0002941; slou.

GO; GO:0005634; C:nucleus; NAS.

GO; GO:0005702; F:RNA polymerase II transcription factor acti. . .; NAS.

GO; GO:0007501; P:mesoderm cell fate specification; NAS.

GO; GO:0007501; P:mesoderm cell fate determination; IEP.

InterPro; IPR001356; Homeobox.

PRINTS; PR00044; Homeobox.

PRODM; PR00010; Homeobox; 1.

SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22010046; PubMed=12015286;
Parker D.S., Jemison J., Cadigan K.M.;
"Pygopus, a nuclear PHD-finger protein required for wingless signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chatterjee S.,
                                                                                                                                                                                                                                                                                          ОНРНААТ ГООНРИ ГО ОРГАЛАЛООНМН-ННОНОН ОНРАНРИЗНОНРИРИРИРИ----
                                                                                                                                                                                                                                                                        QHPHG----ННРН-АННРНЕН ОТНКОН РИСИН РИСИН РИСИН - НРИСИ- НРИСИ - НРИСИ - НРИСИ - НРИСИ - НРИСИ - НРИСИ - НРИСИ -
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MEDLINE-1952490; PubMed=11955446;
MEDLINE-1952490; Pubmed=11955446;
Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee Murone M., Zuellig S., Baaler K.;
Murone M., Zuellig S., Baaler K.;
Wurk,wingless signaling requires BCL9/legless-mediated recruitment pygopus to the nuclear beta-catenin-TCF complex.";
Cell 109:47-60 (2002).
                                                                                                                                                                                                                                                  47;
                                                                                                      PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                            Score 149.5; DB 1; Length 659;
Pred. No. 4.2e-05;
4; Mismatches 49; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                              HIS-RICH.
7 X 2 AM TANDEM REPEATS OF H-P.
POLY-ALA.
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                          5D401F55C4670280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
PYGOOUS protein (Gammy legs protein).
PYGOON GAM OR COIIS18.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                               815 AA
                                                                                                                                                                                       POLY-GLY
                                                                                                                                                                                                                                                                                                                                                         123 LPEANFPSFPLPHHKHPLKPDNQP 146
                                                                                                                                                                                                                                                                                                                                                                            LSP---PTSPAMHSDQQMSPPIAP 278
                                                                                                                                                                                                 HOMEOBOX
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MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                          69955 MW;
                                                                                                                                                                                                                               15.5%;
30.6%;
                                                                                                                                                                                                                                                   44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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542
604
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221
264
364
364
477
536
545
659 AA;
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Best Local Similarity
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Addams M.D. Celniker S.E. Nolt R.A. W. Forms C.A. Googye J.D.,

R. Addams M.D. Celniker S.E. Nolt R.A. W. Forms C.A. Googye J.D.,

R. Goorge R.A. Lowis S. B., Ribardis S., Adhburner W. Henderson S.N.,

B. Sutton G. C. Wortean U.R., Yandell M.D., Shang Q., Chen L.X.,

R. Abile W. W. M. San V. Baxers E.G., Halt G., Chang Q., Chen L.X.,

Ballow M. K. M. San A., Baxers E.G., Halt G., Change M. Pfeiffer B.D.,

B. Harris M. W. Bann A., Baxers E.G., Halt G., Malson C.R., Miklos G.L.G.,

B. Ballow M. W. Bann A., Baxers E.G., Halt G., Malson C.R., Miklos G.L.G.,

B. Burris R.C., Bursan D. Bouck J. By Strekes-Ferminoch C. Black E.B.,

B. Burris R.C., Bursan D. W. Bouck J. By Strekes-Ferminoch C. Black E.B.,

B. Burris R.C., Bursan D. W. Bouck J. By Strekes P. D. Brothow B.C.,

Charry J.W., Carly S., Dahle C., Davenport L.B., Davie B. P.,

Cherry J.W., Carly S., Dahle C., Davenport L.B., Davie B. P.,

Cherry J.W., Carly S., Dahle C., Davenport L.B., Davie B. M.,

Charry J.W., Carly S., Dahle C., Davenport L.B., Davie B. M.,

Charry J.W., Carly S., Daller C., Davenport L.B., Davie B. M.,

Charry J.W., Carly S., Daller C., Davenport L.B., Davie B. M.,

Charry J.W., Carly S., Daller C., Davenport L.B., Davie B. M.,

Charry J.W., Carly S., Daller C., Davenport L.B., Davie B. M.,

Charles D., Boucker A., Deng S., Daller C., Davenport L.B.,

Charles D., Harry D., M., Harry B. M., Maller D., M., M.,

B. M. M., Maller B. W., Carlor C.D., Warger C., Reriez S., Mill D., Lai Z.,

A. Jalai M. K., Abters I. M., Maller T.G., McLed M. M., Maller D.,

B. M. M., Abter B. W., Bettem G. S., Pan S., Pollard J., Puri V., Resee M.G.,

B. M. M., Abter B. W., Bettem G. S., Pan S., Pollard J., Puri V., Resee M.G.,

B. M. M., Abter B. W., Bettem G. S., Chan W., Stypel M., Park S., Wan K.H.,

B. M. M., Abter B. W., Reiner B. M., Woork W., Burksern D. D.,

B. M. M., Maller M., W., Woodys P. W., Kolly K.C., Mang G., San B.,

B. M. M., Marker B. W., Reiner B. W., Woodys B. W., Woodys B. W., Stypel B., Wang G., Wan W.,

B. M. M., Marker B. W., Reiner B
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650
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                                                                                                                                                                                                                                                         8 НЕОН----РИСИНР------НАНИРИЕН ТИКОНРИС---НИРИСИН РИСИНРИСИНР
                                                                                                                                                                                                                                                                                542 HQQHMGGGPPGHGPGPMPGMGMNQMLPPQQPSHLGPPHPNMMNHP--HHPH-HHPGGPPP
                                                                                                                                                                                                                                                                                                             H----GHHPHCHDFQDYGPCDPPPHNQG----HCC---HGH-GPPPGHLRRRG-PGKGP
                                                                                                                                                                                                                                                                                                                                      599 HWMGGPGMHG------GPACMPPHMGGPNPHMMGGPHGNAGPHMGHMGGVPGPGP
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                                                                                                                                                                                                                                  Gaps
GO; GO: 0007367; P: segment polarity determination; IMP.
GO; GO: 0016055; P: Wht receptor signaling pathway; IGI.
InterPro; IPR001965; Znf_PHD.
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
PROSITE; PS01359; ZF_PHD_2; 1.
PROSITE; PS01359; ZF_PHD_2; 1.
Nuclear protein; Trans-acting factor; Wnt signaling pathway; Zinc;
Modal-binding; Zinc-finger; Segmentation polarity protein.

DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97352672; PubMed=9209031; Abbuchi N., Sakurai J.-I., Abbuchi M., Iwahhara O., Ohtani Y., Ohuchi N., Sakurai J.-I., Morita T., Iwahara S., Takegawa K.; Vacuolar Trotein Sorting in fission yeast: cloning, biosynthesis, transport, and processing of carboxypeptidase Y from Schizosaccharomyces pombe."; J. Bacteriol. 179:4179-4189(1997).
                                                                                                                                                                                                                                65;
                                                                                                                                                                                                      15.5%; Score 149.5; DB 1; Length 815; 32.5%; Pred. No. 5.1e-05; ive 7; Mismatches 38; Indels 65;
                                                                                                                                                                                                                                                                                                                                                               99 RPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFP--LPHHKHP 139
                                                                                                                                                                                                                                                                                                                                                                                          O13849; O14366; SIMULARD; FRI; 1002 AH.
O13849; O14366; 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carboxypepidase Y precursor (EC 3.4.16.5) (CPY).
CPYI OR PCYI OR SPACI9G12.10C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetes; Schizosaccharomycetes.
                                                                                                                                                     ASN/GLY/HIS/MET/PRO-RICH.
S -> P (IN REF. 1).
369FD5A5D34BC136 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1002 AA
                                                                                                                                            ALA-RICH
                                                                                                                                                                               80493 MW;
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749
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Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritzc C., Holzer E., Waeller-Auer S.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Purlbert H.,
Borzym K., Zimmermann W., Wadler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Lelaure V., Mottier S.,
Goffeau A., Cadieu E., Dreano S., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,
Daga R.R., Cruzado L., Jimenz J., Sanchez M., Garzon A., Thode G.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Certutti L., Lower T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell BG., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
"The genome involved in degradation of, small peptides. Digests
preferentially peptides containing an aliphatic or hydrophobic
"Esidue in P! Position, as well as methionine, leucine or
phenylalanine in P! position of ester substrate.
"Local All All CALLINY: Release of a C-terminal amino acid with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  broad specificity.
--- SUBBINIT: Heterodimer of two subunits of 32 kDa and 19 kDa derived from the precursor protein and linked by a disulfide bond.
---- SUBCELLULAR LOCATION: Lysosome-like vacuoles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO RICH.
9 X 13 AA TANDEM REPEATS OF M-H-H-E-P-G-
E-H-M-P-P-P-P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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7 X 9 7
G-P-K.
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ACT_SITE
ACT_SITE
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210 РРМНИКРОЕНМРРРРМНИЕРСЕНМРРРМНИЕРСЕНМРРРМНИЕРСЕНМРРРРМНИЕРС 269
                                                                                                                                                                                                                                                                                                                                                        50 HH----PHGHHPHCHDFQDYGPCDPPP--HNQGHCCHGHGPPPGHLRRRGPGRGPRPFHC 103
                                                                                                                                                                                                                                                                                                                                                                                      270 EHMPPPPMHHEPGEH-----MPPPPPMHEPGE----HMPPPPMHEPGEHMPPPPMH- 317
                                                                                                                                                                                                                                                                                   2 РНКНЯЅНЕОН----РНGНИРНАНИР----НЕНDТНRОНРИGНИРНGНН---РНGНИРНG 49
                                                                                                                                                                                                              Ouery Match 15.5%; Score 149.5; DB 1; Length 1002; Best Local Similarity 31.4%; Pred. No. 6.1e-05; Matches 49; Conservative 5; Mismatches 63; Indels 39; Gaps
978 BY SIMILARITY.
924 SUBSTRATE (BY SIMILARITY).
979 SUBSTRATE (BY SIMILARITY).
980 BY SIMILARITY.
982 BY SIMILARITY.
915 BY SIMILARITY.
916 BY SIMILARITY.
917 BY SIMILARITY.
918 BY SIMILARITY.
919 BY SIMILARITY.
910 BY SIMILARITY.
911 BY SIMILARITY.
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9758
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776
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1002 AA;
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Search completed: September 23, 2004, 22:50:35 Job time : 20.2369 secs

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Search time 87.3735 Seconds (without alignments) 534.449 Million cell updates/sec
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1 HPHKHHSHEQHPHGHHPHAH......PSFPLPHHKHPLKPDNQPFP 148
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_fungi:\*
sp\_human:\*
sp\_human:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_organelle:\*
sp\_phage:\*
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sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*

sp\_rvirus:\* sp\_bacteriap:\* sp\_archeap:\*

### Q99ps6 mus musculu Q99ps6 mus musculu Q9ps8 mus musculu Q99ps8 rattus norv Q9bp11 bos taurus Q9ps7 rattus norv Q9esb2 rattus norv Q9esb2 rattus norv Q9esb2 rattus norv Q8mg30 dictryostelli Q9ki87 bacillus ce Q26G56 plasmoduum Q9ki89 bacillus ce Q9ki88 bacillus ce Q7sy91 xenopus lae Q7sy91 xenopus lae Q7sy91 xenopus lae Q1sy12 yenopus Description SUMMARIES 099PS6 099PSB 099PSB 099PSB 099PS7 098PS7 098FS9 098FB9 098FB9 098FB9 098FB9 098FB9 098FB9 098FB9 098FB9 Query Match Length DB Score 6445.5 645.5 644.5 644.5 626.6 626.6 626.7 Result No.

Q8TQB3 Q9YZ77 Q9YK177 Q9YK176 Q9YK191 Q9CK774 Q9CK774 Q9CK774 Q9CK774 Q9CK82 Q9XK82 Q9XK83 Q9XK79 Q9XK79 Q9XK79 Q9XK779 Q9XK781 Q9XX79	OstOb3 drosophila	Q9vsz7 drosophila			Q9ki91 bacillus an	Q9cr74 mus musculu		Q9vv44 drosophila		Q98h88 rhizobium l				Q9ki79 bacillus an	Q81kk8 bacillus an	-	$\boldsymbol{\tau}$	Q89cp3 bradyrhizob	Q9w4c1 drosophila		.4	Q98uk5 brachydanio		Q8r5n0 mus musculu	7			_	P90533 dictyosteli
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# AL IGNMENTS

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RESULT 1 Q99PS6 PRELIMINARY, PRT; 525 AA.	2001 (TrEMBLrel, 17, Creat 2001 (TrEMBLrel, 17, Last	01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Histidine-rich qlycoprotein.	AW413091 OR MAHRG.	Mus musculus (Mouse). Enkamota, Metama, Chordata, Craniata, Vertebrata, Enteleostomi.			SEQUENCE FROM N.A.		Wakabayashi		Submitted	EMBL; AB055897; BAB33094.1; MCD: MCI.0146636; BW413091	GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.	InterPro; IPR000010; Cystatin.	PF00031; cystat	SEQUENCE 525 AA; 59090 MW; A83E93A439CFB3AC CRC64;	66.8%;	Best Local Similarity 69.5%; Pred. No. 7.9e-56; Matches 105; Conservative 9; Mismatches 34; Indels 3; Gaps	1 некиненериенсниенангенеритиконерисинерисиненски	347 НРЫЗИНРРGНИЅИGНИРИGИКРИSНСИНРРGНИРИGНИРИGНИРИСИНРИGНИРИGНИРИGН	61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRK 1	407 DFLDYGPCDPPSNSQELKGQYHRGYGPPHGHSRKRGPGKGLFPFHHQQIGYVYKLPPLNI 4
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SEQUENCE FROM N.A.
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"Murine histidine-rich glycoprotein: cloning, characterization and cellular origin.";
"munol. Cell Biol. 78:280-287(2000).
EMBL; AF194028; AAG28416.1;
"MCD; MGI:2146639; AW413091.
GO; GO:0004869; F:Cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Cystatin.
InterPro; IPR00031; Cystatin; 1.
SMART; SM000043; CY; 2.
SEQUENCE 525 AA; 59132 MM; 6E55F2A439CFB123 CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-UNY-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Histidine-rich glycoprotein.
                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UJW-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein.
                                                                      467 GEVLTLPEANFPSFSLPNCNRSLQPEIQPFP 497
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                                     GEVLPLPEANFPSFPLPHHKHPLKPDNQPFP 148
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TISSUE=Liver;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Submitted (JUL-2001) to the EWBL/GenBank/DDBJ databases.

EMBL; AB055898; BAB33095.1; -.

EMBL; BC011168; AAH11168.1; -.

MGJ; MGI:2146654; AW413091.

GO; GO:00004869; F:cysteine protease inhibitor activity; IEA.

InterPro; IPR00010; Cystatin.

FMART; SM00031; cystatin; 1.

SMART; SM00031; CY; 2.

SEQUENCE 525 AA; 59162 MW; A83E93A439CFB126 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 644; DB 11;
68.6%; Pred. No. 1.1e-55;
iive 7; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 GEVLTLPEANFPSFSLPNCNRSLQPEIQPFP 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 GEVLPLPEANFPSFPLPHHKHPLKPDNOPFP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.5%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TramBlrel, 17, 01-JUN-2001 (TramBlrel, 17, 01-JUN-2003 (TramBlrel, 24, Histidine-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.6
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPRGFRFFHCRQIGSVYRLPPLRKGEV 120
                                                                                                                                                                                               342 HPHGHHPHGQHPHGHHPHGQHPHGH-----HPHGHHLHHPHGHHPHGDHPHGHHPHGH 396
                                                                                                                                                       61 DFQDYGPCDPPPHNQ---GHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRK 117
                                 1 НРНКННЯНЕОНРИСНИРНАНИРИЕНОТИКОНРИСНИРИСНИРИСНИРИСНИРИСНИРИСН
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI TaxID=10116;
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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0TM-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Similar to plasmodium lophurae histidine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hulett M.D., Parish C.R.;
"Murine histidaine-rich glycoprotein: cloning, characterization cellular origin.";
Immunol. Cell Biol. 78:280-287(2000).
BMBL; AF194029; ARG2471.1;
GO, GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Cystatin.
FFam; PF00001; cystatin.
SMART; SMO043; CY: 57581 MW; 508E6E06AA2ED58E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 614.5; DB 11; Length 68.9%; Pred. No. 8.9e-53; tive. 7; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glýcoprotein).
Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                   118 GEVLPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                                                                                                                                                                                                                                                                                                        GEVLTPPEANFPSFSLPNCNRPPQPEIQPFP 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          510
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MEDLINE=20307726; PubMed=10849117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histidine-rich glycoprotein.
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Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=44689;
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Q9ESB2;
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Q9ESB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 HPYGHHPHGHPHDNDFYDHGPCDPPPHRQDPQDHHRQGRDPPPRHSKERGPGKGHFRFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1) - SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-Sprague-Dawley; TISSUB-Liver;

Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.,

Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.,

A. Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;

"Molecular diversity of mammalian histidine-rich glycoprotein.";

"Molecular diversity of mammalian histidine-rich glycoprotein.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB055896; BAB33093.1; -.

RO; Go:0004869; F:cysteine protease inhibitor activity; IEA.

Interpro; IPR00010; Cystatin.

Pfam; PR00031; Cystatin.

Pfam; PR00031; Cystatin.

SRART; SM00043; CY; 2.
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                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                             Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S., Ohashi T., Sato N., Hirata D., Tsuchida N., Kolde T.; Ohashi T., Sato N., Hirata D., Tsuchida N., Kolde T.; Molecular diversity of mammalian histidine-rich glycoprotein."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB055894; BAB33091.1; -
GO, GO:0004865; F:Gysteine protease inhibitor activity; IEA.
InterPro: IPRO00010; Cystain.
Fram; PF00031; Cystain.
SWART; SM00043; CY; 2.
SEQUENCE 546 AA; 61948 MW; 26264858824D89EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 CRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels
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                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 644; DB 6; 62.7%; Pred. No. 1.1e-55;
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                                 546 AA.
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Best Local Similarity 62.74
Matches 104; Conservative
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Best Local Similarity
Matches 105; Conserv
                                                         09BGU1;
01-JUN-2001 (
01-JUN-2001 (
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                                 Q9BGU1
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Q9BGU1
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frame in bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86174893; PubMed=3007981;
Irving D.O., Cross G.A.M., Feder R., Wallach M.;
"Structure and organization of the histidine-rich protein gene of
Plasmodium lophurae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich protein (Fragment)
Plasmodium lophurae.
Bukaryota, Alveolata, Apicomplexa; Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 217; DB 5; Length 140;
Pred. No. 5.3e-14;
2; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  РНХИНЅНЕОНРНСННРНАННРНЕНОТИКОНРНСННРНСННРНСН - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCDI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 AA; 31360 MW; 332D6BC6E0A57A5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA; 18216 MW; ED05EED8C805B2FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 РНСИНРИСИРРИСИВРОЛУСРСВРРИМОСИССИСИ
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EMBL; M15317; AAA29616.1; -.
PIR, A54523; A54523.
NON TER
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                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2003 (TrEMBLrel. 25, Putative VINB (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 39.6
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                   231 HHGHQGQH 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                            95 GKGPRPFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus cereus.
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                 Q26056;
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Q26056
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Q9KI89
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                       Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and Analysis of Chromosome 2 of Dictyostelium."; submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 НРНКНЯ ЗНЕОНРИ СИНГИРИАНИРИЕН ПОТИКОН ----НОСИН-- РИСИ----- НРИС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 НРНКИНЅНЕОНРНСНИРИАНИРИЕНОТИКОНРИСИИРИСИИРИСИИРИСИИРИСИ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=20327579; PubMed=10869077;
Schupp J.M., Klevytska A.M., Zinser G., Price L.B., Keim P.;
"vrrb, a hypervariable open reading frame in bacillus anthracis.";
J. Bacteriol. 182:3989-3997(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----HIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 281.5; DB 5; Length 233;
Pred. No. 3.6e-20;
3; Mismatches 62; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.1%; Score 223.5; DB 2; Length 294; 38.3%; Pred. No. 2.4e-14; ive 5; Mismatches 41; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1396,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC123513; AAM44363.1; -...
EMBL; AC1217070; AAM09303.2; -...
Hypothetial protein.
SEQUENCE 233 AA; 28937 MW; AD4C7A2F86BB14B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 AA; 30753 MW; C05B7B37FE2E395C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LPLPEANFPSFPLPH-HKHPLKPDNQPFP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 ИРНРИРИРИРИРИРИРИРИНИР-ИРИРИРИ 201
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                                                                                                                                                                                                                                               MEDLINE=22092622; PubMed=12097910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.1%;
38.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 38.3
les 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative VrrB (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baumgart C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=AX4;
                                                                                                                                                                                                                           STRAIN=AX4;
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SEQUENCE FROM N.A.
STRAIN=ATCC 31293;
MDDLINB=20237579; DubMed=10869077;
Schupp J.M., Klevytska A.M., Zinser G., Price L.B., Keim P.;
Schupp J.M., Klevytska A.M., Zinser G., Price L.B., Keim P.;
"vrrB, a hypervariable open reading frame in bacillus anthracis.";
J. Bacteriol. 182:3989-3997(2000).
BNBL; PR238897; ARF86202.1;
NON\_TER.

DB 2; Length 273;

SEQUENCE 273 AA; 28573 MW; B80F2979612BEB0C CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 HDFQDYGPCDPPHNQGHCCHGHG-PPPGHLRRRGPGKGPRP-FHCRQIGSVYRLPPLRK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 H------HPPNHTSSEHGSSSEEHTDKKAGKKADRKCFMTRSKGVVQKITLASE 414
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PHGHHPHCHDFQDYGPCDPPPHNQGHCCH-GHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cell-autonomous and signal-dependent expression of liver and intestine marker genes in pluripotent precursor cells from Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JTN-2003 (TrEMBLrel. 24, Created)
01-JTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OTN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Xenopus lastidine-rich protein (Fragment).
Xenopus laevis (African clawed frog)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=22480013; PubMed=12591597;
Chen Y., Jurgens K., Hollemann T., Claussen M., Ramadori G.,
Pieler T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mech. Dev. 120:277-288(2003).

BMBL, AY188284, AAO31610.1, -.

GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

InterPro; IPR00010; Cystatin.

SMART; SM00043; Cyt 2.

Hypothetical protein.
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22.1%; Score 213.5; DB 1.
Best Local Similarity 33.1%; Pred. No. 3.5e-13;
Matches 50; Conservative 12; Mismatches 64
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                                                                                                                                                                                                                                                                                                                                          230 GOHGHHGHQGQHHG 243
                                                                                                                                                                                                                                                                 84 PPPGHLRRRGPGKG 97
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NCBI_TaxID=8355;
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SEQUENCE
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Q801E5;
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DD TO 1-JU
DD TO 1-JU
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                                                                                                                                                                      179 НИНGИНИТИРОАVLYQTHQGQHGHHGH--------НИСЭН--ННОЭНОСНОСНОСНОСТ
                                                                                                                                     46 НРИСИН--------РИСИНРИСНОГО ОУСВРОВРИНОСИСИСИСИВ РРСИГКК
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                                                                    3 НКННSИВОНРИСИРИАНИРИВНDТИКОНРИ-----РИGHI----РИGH-----
                                 47; Gaps
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01-070/2003 (TrEMBLrel. 24, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Similar to fetuin B.
Similar to fetuin B.
Each of African clawed frog).
Eukaryota, Metazoa, Chordeta, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
21.3%; Score 205.5; DB 13; Length 462;
Best Local Similarity 32.5%; Pred. No. 2.2e-12;
Matches 49; Conservative 12; Mismatches 65; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein S., Strausherg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL. BC043891; AAH43891.1; --
EMBL. BC0404869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Cystatin.
Pfam; PR00011; cystatin.
Pfam; PR00011; cystatin.
SMART; SM00043; CY: 2.
SEQUENCE 462 AA; 53185 MW; D7BAD339961739FB CRC64;
                                 Indels
Query Match 21.3%; Score 205.5; DB 2; Best Local Similarity 36.9%; Pred. No. 1.3e-12; Matches 45; Conservative 3; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 GEVLPLPEANF--PSFPLPHHKHPLKPDNOP 146
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                 223 QG 224
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Q7SYH2;
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Q7SYH2
ID Q7SYH
AC Q7SYH
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VRRB. Bacillus cereus. Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus. NCBI\_TaxID=1396;

Last sequence update) Last annotation update)

01-0CT-2000 (TrEMBLEEL 15, 01-0CT-2000 (TrEMBLEEL 15, 01-0CT-2003 (TrEMBLEEL 25, Putative VrrB (Fragment).

Created)

PRELIMINARY;

Q9KI88 Q9KI88;

RESULT 13 Q9KI88

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60 HDFQDYGPCDPPPHNQGHCCHGHG-PPPGHLRRRGPGKGPRP-FHCRQIGSVYRLPPLRK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUBE-Ventral midgut;
Costa R.M.B., Mason J., Lee M., Amaya E., Zorn A.M.;
Novel gene expression domains reveal early patterning of the Xenopus endoderm.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases,
EMBL; AY260732; AAP82289.1; -...
SEQUENCE 462 AA; 53186 MW; 796F92774CC27721 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cystatin domain fetuin-like protein.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TAXID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.3%; Score 205.5; DB 13; Length 462; Best Local Similarity 32.5%; Pred. No. 2.2e-12; Matches 49; Conservative 12; Mismatches 65; Indels 25;
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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 23, 2004, 22:47:25; Search time 26.747 Seconds (without alignments) 285.664 Million cell updates/sec Run on:

US-10-074-225A-5 966 1 HPHKHHSHEQHPHGHHPHAH......PSFFLPHHKHPLKPDNQPFP 148 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

389414 seqs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /cgn2 6/ptcdata/2/laa/5A COMB.pep:\*
2: /cgn2 6/ptcdata/2/laa/5B\_COMB.pep:\*
3: /cgn2 6/ptcdata/2/laa/5A\_COMB.pep:\*
4: /cgn2 6/ptcdata/2/laa/6B\_COMB.pep:\*
5: /cgn2 6/ptcdata/2/laa/PCTUS\_COMB.pep:\*
6: /cgn2 6/ptcdata/2/laa/PCTUS\_COMB.pep:\* Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	nce 64,	Ţ,	'n	equence 2	equence 1	equence (	equence 2	Sequence 25291, A	equence 1		•	٠.	٠.	٠,	•	•	٠.	٠.	Sequence 3, Appli	٠.	• •	• •	28004,	0	equence 24982,	equence 22309,	549,
ΠD	-594-	-785-63	-095-407-	US-09-742-494-2	-09-507-323B-13	-09-543-681A-	-09-252-991A-288	2-9	-09-281-76	-09-507-323B-	9-328-352-65	5-4	US-09-115-032-1		-08-152-9	-406-2	-039A	-461-474-1	-08-686-528A	-09-456-2	US-08-686-528A-2	US-09-456-287-2	US-09-252-991A-28004	US-09-461-474-10	1A-2498	A-2230	US-09-252-991A-25549
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12, Appl 4930, Ap 34, Appl 2019, Ap	100 to 1	26545, A 19317, A 26341, A 28760, A		369, App 407, App 2, Appli 2, Appli
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US-09-461-474-12 US-09-328-352-4930 US-09-602-565-34 US-09-540-236-2019	US-09-461-474-8 US-09-252-991A-26324 US-09-252-991A-22052	US-09-252-991A-26545 US-09-252-991A-19317 US-09-252-991A-26341	US-09-252-991A-2006 US-09-252-991A-27084 US-09-252-991A-24096 US-09-252-991A-22319	US-09-711-164-369 US-09-711-164-407 US-07-882-292-2 US-08-331-644-2
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125 124 123.5	123.5 123.5 120.5	119.5	116.5 116 115.5 115	114.5 114.5 114 114
8 5 5 6 6 8 6 6 6 6	1 C C C C	3 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	8 6 4 4 8 0 0 1	4 4 4 4 0 6 4 0

# ALIGNMENTS

RESULT 1 US-09-76-594-64 US-09-76-594-64 ; Sequence 64, Application US/09976594 ; Patent No. 6673549 ; GENERAL INFORMATION: ; APPLICANT: Furness, Michael · APPLICANT: Furness, Michael	AFFLICANI: TITLE OF INVENTION: GENEE EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REPERENCE: PA-0041 US CURRENT APPLICATION NUMBER: US/09/976,594 CURRENT FILING DATE: 2001-110-12 PRIOR APPLICATION NUMBER: 60/240,409 PRIOR FILING DATE: 2000-10-12 NUMBER OF SEQ ID NOS: 1143 SOFTWARE: PERL PROGRAM SEQ ID NO 64 LENGTH: 525	) TIPE: FAI ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: misc feature ; OTHER INFORMATION: Incyte ID No. 6673549 085596CD1 US-09-976-594-64 Query Match Query Match 98.2%; Score 949; DB 4; Length 525;	yative 0 OHPHGHHPHAH           QHPHGHHPHAH	QY 61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 120	QY 121 LPLPEANPESFPLPHHKHPLKPDNQPFP 148	RESULT 2 US-08-785-636-1 ; Sequence 1, Application US/08785636 ; Patent No. 6027942 ; GENERAL INFORMETT ALTUNG ; APPLICANT: Yip, Tal-Tung ; APPLICANT: Hutchens, T. William
	WITH STEROIDS		60			

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Sequence 13, Application US/09507323B

Patent No. 6274345

GENERAL INFORMATION:

Patent No. 6274345

GENERAL INFORMATION:

APPLICANT: Choi, Jong Hyun

APPLICANT: Lee, Sang Yup

APPLICANT: Lee, Sang Yup

APPLICANT: Lee, Sang Yup

TITLE OF INVENTION: ENCODING OMPC DERIVED FROM B.COLI AS CELL SURFACE ANCHORING

TITLE OF INVENTION: MOTIF

TITLE OF INVENTION: MOTIF

TITLE OF INVENTION: WOTIF

TITLE OF INVENTION: WOTIF

TITLE OF INVENTION NUMBER: US/09/507,323B

CURRENT PELLIAG DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 167

TYPE: RET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HUTCHENS, WILLIAM
APPLICANT: HUTCHENS, WILLIAM
APPLICANT: HUTCHENS, WILLIAM
TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES
FILE REFREENCE: P00798USE/09306611
CURRENT APPLICATION NUMBER: US/09/742,494
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
LENGTHA: 26
LENGTH: 26
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19.1%; Score 184.5; DB 3; Length 167;
Best Local Similarity 32.7%; Pred. No. 5.6e-11;
Matches 48; Conservative 2; Mismatches 50; Indels 47.
                                                            Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 --PHGHHPHGH---HPHGHHPHGH---HPHGHHPHCHDFOD----
                                                            Score 185; DB 3; I
Pred. No. 6.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 185; DB 4;
Pred. No. 6.9e-12;
                                  19.2%; bccc. No. c. 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
19.2%; Score 185; DB
Best Local Similarity 100.0%; Pred. No. 6.9
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HPHKHHS-----HEQH----PHGHH---
                                                                                                                                                                                                                                                      1 GHHPHGHHPHGHHPHGHHPH 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 СНИРИСНИРИСНИРИСНИРИ 58
                                                                                                                                                                                                     34 СИНРИСИИРИСИИРИСИИРИСИИРИ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), OTHER INFORMATION: Histidine linker. US-09-507-323B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09742494 Patent No. 6528320
                                                        Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-494-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-507-323B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yip, Tai-Tung
TITLE OF INVENTION: Surface-Enhanced Neat Desorption for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,407
FILING DATE: 10-Jun-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/068,896
FILING DATE: 28-MAY-1993
APPLICATION NUMBER: WO PCT/US94/06064
FILING DATE: 27-MAY-1994
APPLICATION NUMBER: US 08/556,951
FILING DATE: 27-MOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 185; DB 3; Length 26;
Pred. No. 6.9e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Unknown Organism:
US-08-785-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5639-PCT-US-D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-5325
TELEFAX: (713) 651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 MCKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of Analytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.2%; Score 185; DB Best Local Similarity 100.0%; Pred. No. 6.9 Matches 25; Conservative 0; Mismatches
FILE REPERENCE: Hutchens
CURRENT APPLICATION NUMBER: US/08/785,636
CURRENT FILING DATE: 1997-01-17
EARLIER APPLICATION NUMBER: 08/068,896
EARLIER FILING DATE: 1993-05-28
SOFTWARE: PatentIn Ver: 2.0
SOFTWARE: PatentIn Ver: 2.0
LENGTH: 26
TYPE: PATENTER
CORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; STRANDEDNESS: «Unknown»; TOPOLOGY: linear MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-095-407-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHHPHGHHPHGHHPHGHHPH 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09095407
Patent No. 6124137
GENERAL INFORMATION:
APPLICANT: Hutchens, T. William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-095-407-2
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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38 RHPAGHRPHRLGQDHHPVRQPDHAQRPHAEHPHRRGSDRIPPGGHRPDPGQRQGRHDLRP 97

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GENERAL INFORMATION:

### PAPLICATION US/09252991A

### PAPLICATION US/09252991A

### PAPLICATION US/09252991A

### PAPLICATION:

### PAPLICATION:

### PAPLICATION:

### PAPLICATION UNDER:

### PAPLICATION UNDER:

### PAPLICATION UNDER:

### PAPLICATION UNDER:

### PRIOR FILING DATE:

### PRIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 ААГНУНСНААУННЯКНІСАУАВІЛАНУНАНКЯНІЛАОНАУУНКРАІНС----КНЯНКНА 180
                                                                                                                           98 RPAGDPPAGPGRGDGRRDPRPGDRRDRGAGFADRPPGALDPAHQQRHRCDHPPGGHGHRA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ненсинен--синрисногорусрсоврениосис 78
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US-09-281-766-19

US-09-281-766-19

Sequence 19, Application US/09281766

Patent No. 6376196

APPLICANT: Louie, Kitland

APPLICANT: Toule, Kitland

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Recombinant Neospora Antigens and Their Uses

FILE REPRENENT: 1990-03-30

CURRENT APPLICATION NUMBER: US/09/281,766

PRIOR APPLICATION NUMBER: US/09/281,766

NUMBER OF SEQ ID NOS: 23

SOUTHARE: PatentIN Ver. 2.1

SEQ ID NO 19

LENGTH: 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.4%; Score 158.5; DB 4; Length 218;
Best Local Similarity 30.7%; Pred. No. 2.7e-08;
Matches 46; Conservative 5; Mismatches 50; Indels 49
                                                                                                                                                                                                  85 PPG---HLRRRG--PGKGPRPFHCRQIGSVYRLPPLRKGEV 120
                                                                                                                                                                                                                                                                     158 VPAVLLHAWRAGPAPGAGALP-----GVQGALPRRGRV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 нісіняндсінункніндіннодивскиз 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Neospora sp. ) OTHER INFORMATION: NC-p65 cDNA US-09-281-766-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 ----HGH----HDHCH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HPHKHHSHEQHP---
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US-09-252-991A-28819
Sequence 28819, Application US/09252991A
Fatent No. 6551795
GENERAL INFORMATION:
FATELE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPREBENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
FRICR APPLICATION NUMBER: US 60/074,788
FRICR APPLICATION NUMBER: US 60/074,190
FRICR FILING DATE: 1998-07-18
FRICR APPLICATION NUMBER: US 60/094,190
FRICR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28819
LENGTH: 225
                                                                                                                                                                                                                                                                                                              Sequence (151, Application US/09543681A)

Sequence (151, Application US/09543681A)

Sequence (151, Application US/09543681A)

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

TITLE OF INVENTION: US/09/543,681A

FILE REFERENCE: 2709.1002-001

CURRENT FAPILICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6151

LENGHH 400
68 LDPSGHHHHHHSGLDPSGHHHHHHSGLDPSGHHHHHSGLDPSGHHHHH11111 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 GQPIIIHHHYHNSGDVHLHFYHDAQQNEAQVFНЕННЫӨНDЫНAHSHEHTHSHEHSH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---HPHG----HHPHGH-HPHGH-+PHCH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.9%; Score 172.5; DB 4; Length 400; Best Local Similarity 29.9%; Pred. No. 2.1e-09; Matches 41; Conservative 4; Mismatches 23; Indels 69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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16.7%; Score 161.5; DB 4;
Best Local Similarity 32.3%; Pred. No. 1.4e-08;
Matches 52; Conservative 3; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 НРНКННS--НЕОНРНGННРНАННРНЕ-НDTHROH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 нн--нясгорафининизоразсни 152
                                                                                                    76 GHCCHGHGPPPGHLRRRGPGKGPRPFH 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DFQDYGPCDPPPHNQGH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 G----HHPHGH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-28819
                                                                                                                                                                                                                                                                                        RESULT 6
US-09-543-681A-6151
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                                         임
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Gaps

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132 НGHHLHRRHHNGCGHGLDRLNGHGHHLHRRHHNGCDHGLGHLNGHDHHLHRRH-HGGCGH 190
                                                                                                                                                                                                                                             191 DFGHLSDRDHHLHRRH-HGGCGHDLDRLNDRDHHLHRRH-HGGCDHDLGHLNDRDHHLHR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AHHEEQHGGH--HHHHHHHHHHHYHGGEHHHHHHSSHH------EEGCCSTSDSHHQEE 52
                                                                                                              ---РНСНИРНАНН------РНЕНОТНКОНРНС---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           АННРНЕНОТНКОНРНGHHPHGHHPHGHHPHGHHPHGHHPHCHDFQDYGPCDPPP--HNQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 11; Gaps
                                                                 90;
                                                                                                                                                                                                                                                                                                                             H----HHGCD----HGLGHLSDRDHHLRRHHDCDHGHDRLSDRDHHLRR 290
                                                                                                                                                                                                                                                                                            ....----CCHGH---GPPPGHLRR 91
                       Score 147; DB 4; Length 339;
Pred. No. 5.7e-07;
4; Mismatches 28; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELICOBACTER PYLORI NICKEL BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 15.0%; Score 144.5; DB 1, Best Local Similarity 40.9%; Pred; No. 1.6e-07; Matches 27; Conservative 3; Mismatches 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Daut, Andrew G.
APPLICANT: Gilbert-Rothstein, Joanne V.
APPLICANT: Wright, Andrew
APPLICANT: Wright, Andrew
TITLE OF INVENTION: HELICOMACTER PYLORI NI
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STRAET: Wassachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00398/090001
                                                                                                                                                                                                                                                                                                                                                                                                                                              . Sequence 1, Application US/08255457; Patent No. 5780040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAK: (617) 542-8906
                                                                                                                                                                                                     35 -----HHPHGHHPHG-
                       15.2%;
llarity 27.8%;
Conservative
                                                                                                                                                                                                                                                                                            60 HDFQDYGPCDPPPHNQGH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
                                                                                                                3 HKHHSHEQH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-255-457-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                            L Similarity
47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 HCCHGH 82
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53 GCCHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-255-457-1
                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                 Best Local
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Choi, Jong Hyun
APPLICANT: Choi, Jong Hyun
APPLICANT: Lee, Sang Yup
TITLE OF INVENTION: EXPRESSION VECTORS COMPRISING A GENE
TITLE OF INVENTION: ENCOING OMPC DERIVED FROM B.COLI AS CELL SURFACE ANCHORING
TITLE OF INVENTION: MOTIF
TITLE OF INVENTION: MOTIF
FILE REFERENCE: HYLEE39.001AUS
CURRENT APPLICATION NUMBER: US/09/507,323B
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: KR 10-1999-0005773
PRIOR PELING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FARFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: BAUGHOUS ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUGHOUS IN DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6551
LENGTH: 339
                                               9
                                                                                                                          571 PDRQHPHPHPRPNPPEASPPEPSPNWQHPHPHPRPNPPEASPPEPSPPNWQHPHPHP 630
                                                                                                                                                                              62 FQDYGP-CDPP---PHNQGHCCHGHGPPPGHLRRRGPGKGP----RPF----HCRQIGSV 109
                                                                                                                                                                                                                        631 PRPNPPGASPPESSPNWQH-PHPHPPRPNPPEASPPOSSPPEPORPFSQWPHTPHFFHY 689
                                                                                           61
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                                                                                         2 РНКИНЅНЕОНРИСНИРИАНИРИЕНОТИКОНРИСНИРИСНИРИСНИРИСНИРИСНИРИСНИР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                нянния драгининия драгининия -- драгининия драгининия
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
  Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 148.5; DB 3; Length 8 Pred. No. 9.9e-08; 0; Mismatches 27; Indels
                                               88; Indels
                                                                                                                                                                                                                                                                  110 YRLP----PLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQP 146
                                                                                                                                                                                                                                                                                                             690 HPYPGYNLPYFTYHQSPLPYGPYGRDPCPCASHPYPADDSP 730
DB 4;
16.1%; Score 155.5; DB 4
29.2%; Pred. No. 2.3e-07;
iive 9; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6551, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Histidine linker. JS-09-507-3238-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-6551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.5%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 ---НРНGННРНСН 60
                                               47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 SGLDРSGHНННН 78
                     Best Local Similarity
Matches 47; Conserv
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US-09-328-352-6551
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LENGTH: 89
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  Query Match
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Knapp, Bernhard
APPLICANT: Hundt, Erika
APPLICANT: Hundt, Erika
APPLICANT: Enders, Burkhard
APPLICANT: Enders, Burkhard
APPLICANT: Enders, Burkhard
APPLICANT: Kuepper, Hans
TITLE OF INVENTION: Apprid Proteins which Contain Part-Sequences of the Malaria
TITLE OF INVENTION: Apprid Proteins which Contain Part-Sequences
TITLE OF INVENTION: Apprid Proteins which Contain Part-Sequences
TITLE OF INVENTION: Antigens HRPII and SERP, the Preparation and Use Thereof
NUMBER OF SEQUENCES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W. Suite 700
CITY: Washington
STREET: D.C.
ZIP: ZO005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCATION DATA:
APPLICATION NUMBER: US/08/152,922A
FILING NUMBER: LAGANGUES WANDV-1903
FILING NUMBER: LAGANGUES WANDV-1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 АННРНЕНДТИКОНРНСНИРНСНИРНСНИРНСНИРНСНДГОДУСРСДРРР--НИОС 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 11; Gaps
                             COUNTRY: W.S.A.

ZIP: 02110-2804

ZIP: 02110-2804

COUNTRY: U.S.A.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05772
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark Paul C.
REFIERENCE/DOCKET NUMBER: 00398/090001
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELEPAX: (617) 542-8906
TELEFEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LANDER THE COMPANIENT OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LANDER THE COMPANIENT OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LANDER THE COMPANIENT OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LANDER THE COMPANIENT OF SEQ ID NO: 1:
AND THE COMPANIENT OF SEQ ID NO: 1:
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LANDER THE COMPANIENT OF SEQ ID NO: 1:
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Pred. No. 1.6e-07;
3; Mismatches 25;
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; Sequence 6, Application US/08152922A
; Patent No. 5395614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.9%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-05772-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AHHEEQHGGH--HHHHHHHHHHHHHHHHHHHSSHH-----EEGCCSTSDSHHQEE 52
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                                                                                                                                                                                                                          APPLICANT: Plaut, Andrew G.
APPLICANT: Gilbert-Rochstein, Joanne V.
APPLICANT: Wright, Andrew
APPLICANT: WRIBH, Andrew
ITILE OF INVENTION: HELICOBACTER PYLORI NICKEL BINDING
ITILE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/115,032

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/255,457

FILING DATE:

ATTOMNY AGENT INFORMATION:

NAME: Clark, Paul C:

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

RETERENCE/DOCKET NUMBER: 00398/090011

TELECOMMUNICATION INFORMATION:

TELEPRAK: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Plant, Andrew G.

APPLICANT: Gilbert-Rothstein, Joanne V.

APPLICANT: Wright, Andrew

TITLE OF INVENTION: HELICOBACTER PYLORI NICKEL

TITLE OF INVENTION: BINDING PROTEIN

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSES:

STREET: 225 Franklin Street
CITY:
Boston
STREET: 425 Franklin Street
CITY:
Boston
STREET: 226 Franklin Street
CITY:
Boston
STREET: 226 Franklin Street
CITY:
Boston
STREET: 226 Franklin Street
CITY:
Boston
STREET: 120 Franklin Street
COUNTER: 120 Franklin Street
COUNTER: 120 Franklin Street
COMPUTER: 120 Franklin PC-00 Fr
                                                                                              Sequence 1, Application US/09115032
Patent No. 5972348
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 GCCHGH 58
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PCT-US95-05772-1
RESULT 13
US-09-115-032-1
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| FILING DATE: 13-DEC-1991
| CLASSIFICATION: 424
| ATTORNEY/AGENT INFORMATION:
| NAME: Eliaudi, Carol P. |
| REFREENCEDOCKET NUMBER: 32,220
| REFREENCEDOCKET NUMBER: 02481-1143-02000
| TELEPHONE: 202-408-4000
| TELEPHONE: 202-408-4000
| TELEPHONE: 202-408-4000
| TELEPHONE: 202-408-4000
| INFORMATION FOR SEG ID NO: 6: SEQUENCE CHARACTERISTICS:
| LENOTH: 189 amino acids | TYPE: amino a
```

Search completed: September 23, 2004, 22:56:48 Job time: 27.747 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

September 23, 2004, 22:55:11; Search time 101.044 Seconds (without alignments) 470.989 Million cell updates/sec 1 HPHKHHSHEQHPHGHHPHAH........PSFPLPHHKHPLKPDNQPFP 148 1349238 seqs, 321558718 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-074-225A-5 Title: Perfect score: Scoring table: Sequence: Searched: Run on:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published Applications AA:\*

1: \cgn2\_6/ptodata/2/pubpaa/USO7\_PUBCOMB.pep:\*
2: \cgn2\_6/ptodata/2/pubpaa/USO7\_NEW PUBL.pep:\*
3: \cgn2\_6/ptodata/2/pubpaa/PCTNEW PUBL.pep:\*
4: \cgn2\_6/ptodata/2/pubpaa/USO6\_NEW PUB.pep:\*
5: \cgn2\_6/ptodata/2/pubpaa/USO6\_NEW PUB.pep:\*
5: \cgn2\_6/ptodata/2/pubpaa/NSO7\_NEW PUB.pep:\*
6: \cgn2\_6/ptodata/2/pubpaa/PCTUG\_PUBCOMB.pep:\*
7: \cgn2\_6/ptodata/2/pubpaa/NSO8\_NEW PUB.pep:\*
8: \cgn2\_6/ptodata/2/pubpaa/NSO8\_NEW PUB.pep:\*
9: \cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
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18: \cgn2\_6/ptodata/2/pubpaa/USO8\_NEW\_PUB.pep:\*
18: \cgn2\_6/ptodata/2/pubpaa/USO8\_NEW\_PUB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Sequence 5, Appli	Sequence 1, Appli	Sequence 62, Appl	Sequence 3, Appli	Sequence 166051,	Sequence 1, Appli	Sequence 6, Appli	Sequence 33892, A	Sequence 37944, A	Sequence 9, Appli	Sequence 13, Appl	Sequence 33313, A	Sequence 2423, Ap		Sequence 2422, Ap
ID	US-10-074-225A-5	US-10-074-225A-1	US-09-919-039-62	US-10-074-225A-3	US-10-424-599-166051	US-09-730-379B-1	US-10-074-225A-6	US-10-029-386-33892	US-09-864-761-37944	US-09-730-379B-9	US-09-730-379B-13	US-09-864-761-33313	US-10-389-566-2423	US-10-389-566-2424	US-10-389-566-2422
DB	14	14	10	14	12	σ	14	14	σ	σ	σ	σ	16	16	16
Query Match Length DB	148	525	525	526	67	75	101	378	292	38	38	82	130	133	265
Query Match	100.0	100.0	98.2	56.2	33.6	31.3	29.0	25.1	22.9	22.0	22.0	21.7	20.7	20.7	20.7
Score	996	996	949	543	325	302	280.5	242.5	221	213	213	210	199.5	199.5	199.5
Result No.	П	7	ĸ	4	2	9	7	∞	6	10	11	12	13	14	15

Sequence 281824,	Seguence 41679, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 37352, A	Seguence 45941, A	Sequence 33727, A	Seguence 34744, A	Sequence 825, App	Sequence 69999, A	Sequence 186228,	Sequence 160290,	Sequence 1014, Ap	Seguence 130, App	Sequence 37882, A	Sequence 31185, A	Sequence 14106, A	Sequence 33, Appl	Sequence 76, Appl	Sequence 122803,	Sequence 33860, A	363,	363,	Sequence 198315,	7758	13228,	Sequence 19, Appl	Sequence 4, Appli
-28	US-09-864	US-09-809-657-2	9 US-09-848-512A-2	US-09-742	US-1	0S-09	0-282-122A	0S-09	US-09-864-761-34		N	N	a	14 US-10-083-357-1014	US-09-830-688		US-10-029-386	US-10-156-761	15 US-10-360-849A-33	US-10-406-686	US-10-437-963-1	US-10-029-386-3	12 US-10-221-278-363	US-10-291-172-3	US-10-437-963-1	14 US-10-032-585-7758	761-1	-957	J.
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19.9	19.8	19.2	19.2	19.2		•		18.6	18.6	18.5	18.1	17.8	17.8	17.2	17.0	17.0	17.0	17.0	16.8	16.6	16.4	16.4	16.4	16.4	16.3	16.2	16.1	16.1	16.0
192.5	191.5	185	185	185	185	185	182	179.5	179.5	178.5	175	172	171.5	166	164.5	164	164	164	162	160.5	158	158	158	158	157	156.5	155.5	155.5	155
16	17	18	13	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37		39	40	41	42	43	44	45

## ALIGNMENTS

APPLICANT: DONATE, Fernando
APPLICANT: DONATE, Fernando
APPLICANT: PLUNKETT, Marian L
APPLICANT: PLUNKETT, Marian L
APPLICANT: HARRIS, Scott
TILLE OF INVENTION: HISTIDINB PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC
TILLE OF INVENTION: ANTI-TUMOR AGENT
FILE REFERENCE: 38342-178463
FURRENY FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/268,370
PRIOR PLING DATE: 2001-02-14
PRIOR PLING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
SOFTWARE: PRIOR DATE: COURTH: 148
TYPE: PRI
CORGANISM: Home sapiens 1 неикнизивонириснирианиривнотиконириснириснириснириснириснирисн Gaps 0; Length 148; Indels Query Match 100.0%; Score 966; DB 14; Best Local Similarity 100.0%; Pred. No. 1.4e-69; Matches 148; Conservative 0; Mismatches 0; Sequence 5, Application US/10074225A Publication No. US20030082740A1 GENERAL INFORMATION: US-10-074-225A-5 qq g 8  $\delta$ 

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LPLPEANFPSFPLPHHKHPLKPDNOPFP 148

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APPLICANT: DONATE, Fernando
APPLICANT: DIUNKETT, Martan L
APPLICANT: BLUNKETT, Martan L
APPLICANT: HARRIS, Societ
APPLICANT: HARRIS, Societ
APPLICANT: HARRIS, SOCIET
APPLICANT: HARRIS, Andrew P
TITLE OF INVENITON: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC J
TITLE OF INVENITON: ANTI-TUMOR AGENT
FILE SPERENCE: 38342-174863
CURRENT APPLICATION NUMBER: US/10/074,225A
PRIOR APPLICATION NUMBER: US 60/268,370
PRIOR PLING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOCIETATION NOS: 11
SOCIETATION OF SEQ ID NOS: 11
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 166051, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREMENTS: 163213) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 166051
LENGTH: 67
350 НРНКНИЅНЕОНРИСНИРИАНИРИЕН ОТИКОНРИСНИРИСКИРИСНИРИСКИРИСКИ 409
                                                                  61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 543; DB 14;
Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches
                                                                                                                                                                                                   121 LPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                                                                                                                                                                                                                             470 LPLPEANFPSFPLPHHKHPLKPDIQPFP 497
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10074225A Publication No. US20030082740A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 РНКННЅНЕОНРИСИНРНА--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.6%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Lepus americanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: unsure
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                                                                                                                                                         Sequence 1, Application US/10074225A

Sequence 1, Application No. US20030082740A1

GENERAL INPORMATION:

APPLICANT: DONATE, Fernando

APPLICANT: PLUNKETT, Marian L

APPLICANT: HARRIS, Scott

APPLICANT: HARRIS, Scott

APPLICANT: HARRIS, Scott

TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC

TITLE OF INVENTION: ANTI-TUMOR AGENT

TITLE OF INVENTION: ANTI-TUMOR AGENT

TITLE OF INVENTION: NUMBER: US/10/074,225A

CURRENT APPLICATION NUMBER: US 60/268,370

PRIOR FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 1

LENGTH: S25

TYPE: PRT

CREMINEN: PARCHINEN SECOND 3.1

SEQ ID NO 1

SEQ ID NO 1
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US-09-119-039-62
US-09-119-039-62

| US-09-119-039-62
| Publication No. US20030108871A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Kaser, Matthew R. |
| TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES CURRENT APPLICATION NUMBER: US/09/919,039
| CURRENT APPLICATION NUMBER: US/09/919,039
| PRIOR FILING DATE: 2002-09-09
| PRIOR FILING DATE: 2000-07-28
| NUMBER OF SEQ ID NOS: 401
| SOFTWARE: PERL PROGram
| SEQ ID NO 62
| LENGTH: 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 НРНКНИЅНЕОНРИСИНРНАНИРИВНОТИКОНРИСИИРИСИИРИСКИРИСКИРИСКИРИСК
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; OTHER INFORMATION: Incyte ID No. US20030108871A1 085596CD1
US-09-919-039-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 966; DB 14; Best Local Similarity 100.0%; Pred. No. 4.4e-69; Matches 148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.6%; Pred. No. 9.9e-68;
Matches 146; Conservative 0; Mismatches 2;
          121 LPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LPLPEANFPSFPLPHHKHPLKPDNOPFP 148
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ORGANISM: Homo sapiens
                                                                                                        RESULT 2
US-10-074-225A-1
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g  $\delta$ 

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DENEKAL INFORMATION.

APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David R.
TITLE OF INVENTION: *EXPRESSION ANALYSIS TWO
CURRENT PELLING DATE: 2001-12-20
UNRENT PELLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFFWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33892
LENGTH: 378
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL, FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
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                                                                                                                            19;
                                                                          DB 14; Length 101;
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                                                                       Score 280.5; DB 14; Length
Pred. No. 3.8e-15;
1; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: MAP TO AP001751.1
INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.6
INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
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47.1%; Pred. No. 1.4e-11;
tive 1; Mismatches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33892, Application US/10029386; Publication No. US20030194704A1; GENERAL INFORMATION:
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Patent No. US20020048763A1
                                                                                                                                                                              2 РНКНИЅНЕОНРИСИНРИА---
                                                                       Query Match
Best Local Similarity 51.6%;
Matches 47; Conservative
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Best Local Similarity 47.14
Matches 41; Conservative
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ORGANISM: Homo sapiens
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CTHER INFORMATION
US-10-029-386-33892
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                        US-10-074-225A-6
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| Sequence 6, Application US/10074225A |
| Publication No. US2030082740A1 |
| Publication No. US2030082740A1 |
| GENERAL INFORMATION |
| APPLICANT: DONATE Fernando |
| APPLICANT: PLUNKETT, Marian L |
| APPLICANT: HARIS, Scott |
| TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC |
| TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC |
| TITLE OF INVENTION: ANTI-TUMOR AGENT |
| FILE REFERENCE: 38342-178463 |
| CURRENT APPLICATION NUMBER: US 60/268,370 |
| PRIOR APPLICATION NUMBER: US 60/268,370 |
| PRIOR FILING DATE: 2001-02-14 |
| NUMBER OF SEQ ID NOS: 11 |
| SOFTHARE: Patentin Version 3.1
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                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09730379B
Patent No. US20010041670A1
GENERAL INFORMATION:
APPLICANT: Sinantcv M.D., Ronit
APPLICANT: Silverstein M.D., Roy L.
TITLE OF INVENTION: THROMBOSPONDIN-BINDING REGION OF HISTIDINE-RICH
TITLE OF INVENTION: CLYOPROTEIN AND METHODS OF USE
FILE REFERENCE: 955-7P/CON
CURRENT APPLICATION NUMBER: US/09/730,379B
CURRENT APPLICATION NOWNER: 2000-12-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                   17 HPHYCHSQHPGHPHAHHPHSHDTHRQHPHGHHPXGNHPHGHTPHGGH 67
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                                                                                                                                                                                                                          Indels
                                                                                                                                                                              Length
                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_120960C.1.pep
US-10-424-599-166051
                                                                                                                                                                           Score 325; DB 12;
Pred. No. 7.4e-19;
1; Mismatches 3;
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PUBLICATION INFORMATION: PUBLICATION INFORMATION
JOURNAL: Biochemistry
VOLUME: 25
LOCATION: (1)..(67)
CTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATABASE ACCESSION NUMBER: GenBank/P04196
                                                                                                                                                                        Query Match
Best Local Similarity 92.2%;
Matches 47; Conservative
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Matches 52; Conserv
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DATE: 1986
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US-09-730-379B-1
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LENGTH: 101
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LENGTH: 75
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Local Similarity
nes 38; Conserv
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PAGES: 2220-2225
DATE: 1986
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US-09-730-379B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 НКННЅНЕОНРИGHИРНАНИРНЕНОТИКОНРИGНИРНGHИРНGH-ИРНСНИРНСНО
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US-09-730-379B-9

Sequence 9, Application US/09730379B

Patent No. US20010041670A1

GENERAL INFORMATION:

APPLICANT: Sinantow M.D., Ronit

APPLICANT: Silverstein M.D., Roy L.

TITLE OF INVENTION: THYORMSOEONDIN BINDING REGION OF HISTIDINE-RICH

TITLE OF INVENTION: GLYCOPROTEIN AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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OTHER INPORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.5

OTHER INPORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BT411, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.9

US-09-864-761-37944
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PPLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PPLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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ORGANISM: Homo sapiens
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Matches 41; Conserva
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LENGTH: 292
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Sequence 33313, Application US/09864761
Factor No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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APPLICANT: Silverstein M.D., Roy L.
APPLICANT: Silverstein M.D., Roy L.
TITLE OF INVENTION: THROMBOSPONDIN-BINDING REGION OF HISTIDINE-RICH
TITLE OF INVENTION: GLYCOPROTEIN AND METHODS OF USE
FILE REFERENCE: 955-7P/CON
CURRENT APPLICATTON NUMBER: US/09/730,379B
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 13
LENGTH: 38
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FILE REFERENCE: 955-7P/CON
CURRENT APPLICATION NUMBER: US/09/730,379B
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 13
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 9
ILENGTH: PR
CREAVISM: Homo sapiens
CREAVISM: Homo sapiens
JOURNAL: Biochemistry
VOLUME: 25
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ilarity 100.0%; Pred. No. 3.7e-10;
Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION: PUBLICATION INFORMATION
JOHENAL: Biochemistry
VOLUME: 25
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DATE: 1986
DATABASE ACCESSION NUMBER: Genbank/P04196
                                                                                                                                                                                                                                                                                                                                                                                  DATABASE ACCESSION NUMBER: GenBank/P04196
US-09-730-3798-9
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APPLICANT: Monsantor Technology, LLC
APPLICANT: Laurie, Cathy C
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77 (22900) D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin Version 3.2
SEQ ID NO 2424
              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR PILLING DATE: 2002-06-25
PRIOR PILLING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin Version 3.2
SEQ ID NO 2423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 НРНКИНЅНЕОНРИСИНРИАНИРИЕНОТИКОНРИ-СИИР-СИИ-РИСИИР----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 НРИКНИЅНЕОНРИСИИРИАНИРИЕНОТИКОИРИ-СИИРИ-СИИРИ-СИИ-РИСИИР----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.7%; Score 199.5; DB 16; Length 133; 44.6%; Pred. No. 1.4e-08; tive 2; Mismatches 35; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 199.5; DB 16;
Pred. No. 1.3e-08;
2; Mismatches 35;
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; Sequence 2424, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.6%;
Matches 45; Conservative
US20040025202A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bacillus anthracis
US-10-389-566-2423
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US-10-389-566-2424
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Best Local Similarity
Matches 45; Conserva'
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N: EXPRESED IN FETAL LIVER, SIGNAL = 7
N: EXPRESED IN HELA, SIGNAL = 8.1
N: EXPRESED IN ADULT LIVER, SIGNAL = 7.5
N: EXPRESED IN PLACENTA, SIGNAL = 9.5
N: EXPRESED IN UNG, SIGNAL = 9.5
N: EXPRESED IN HEART, SIGNAL = 9.5
N: EXPRESED IN BRAIN, SIGNAL = 9.2
N: EXPRESED IN BRAIN, SIGNAL = 9.2
N: EXPRESED IN BONE MARROW, SIGNAL = 6.1
N: EXPRESED IN HOME MARROW, SIGNAL = 6.1
N: EXPRESED IN HIT: Q12329, EVALUE 4.900+00
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY ELIE REFERENCE: Accomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                         CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PELING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-36

PRIOR PILING DATE: 2000-06-36

PRIOR PILING DATE: 2000-06-36

PRIOR PILING DATE: 2000-09-27

PRIOR PELING DATE: 2000-10-49

PRIOR PELING DATE: 2000-10-40

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 09/744,203

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR PELING DATE: 2001-01-29

PRIOR PELING DATE: 2001-01-29

PRIOR PELING DATE: 2001-01-29

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-29

PRIOR PELING DATE: 2001-01-29

PRIOR PELING DATE: 2001-01-2
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Best Local Similarity 56.9°
Matches 33; Conservative
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FEATURE:
OTHER INFORMATION: MAPOTHER INFORMATION: EXPOTHER 
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ORGANISM: Homo sapiens
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RESULT 13 US-10-389-566-2423 ; Sequence 2423, Application US/10389566

нненн-нінродігуотн----однодниринсински 103

53 -НGHHPHCHD-----FQDYGPCDPPHNQGHCCHGHGPPPGH 88

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OBSTOLATION OF US2004002520241

Sequence 2422, Application US/10389566

Publication No. US2004002520241

SEQUENCE THORMATION:
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Search completed: September 23, 2004, 23:11:16 Job time : 103.044 secs

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(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

September 23, 2004, 21:23:24 Run on:

4 ; Search time 68.9558 Seconds (without alignments) 413.849 Million cell updates/sec

US-10-074-225A-6

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

genescqp20008:\* genescqp20018:\* genescqp20038:\* genescqp2003as:\* genescqp2003bs:\* genescqp2003bs:\* A\_Geneseq\_29Jan04:\* .: geneseqp1980s:\* ?: geneseqp1990s:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Abb7980	9804	897 Human I			Abg09949 Novel hum	Ra	5 Rat	0 Rat	Prot		ORF1 o	Human	Abo52997 Human spl	Aao30246 Human Sap	Aao30188 Human cP3	Aao30408 Human sec	Aaw50192 Amino aci	Aab71667 Human col	4	Abb68218 Drosophil	Abull891 Human ABC	183	1362	Abp73921 Candida a
ΙD	ABB79805	ABB79804	ADE76897	ABB79807	ABB79806	ABG09949	ADD45442	ADE57105	ADD47240		AAR04119	AAR04116	ADD45740	AB052997	AA030246	AA030188	AAO30408	AAW50192	AAB71667	AAB71654	ABB68218	ABU11891	ABB61183	ABB61362	ABP73921
Length DB	26	25	25	48	148 5	91	96	96	74	74	74	60	31	24	~	80	67	24	m	۳	020	7	80		1130 5
강	100.0	45.1	45.1	•	40.2	7	•	37.2	ď.		m.	m.	ω.		m.		ω.	ď	ď				32.3		32.0
Score	697	314	314	80	0	64.	59.	59	4	246	233.5	233.5	233.5	233.5	231.5	231.5	231	229.5	ω.	228.5	œ.	22	225	223	223
		N	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Abb78538 Ser-Pro-P		o Ant	0	_	Abb70499 Drosophil	Abp54340 Drosophil	App43151 Human ova		Aaw50193 Amino aci		Adc87177 Human GPC	ιn	Abb62915 Drosophil	Aar12362 Octopus r	Aau28194 Novel hum	Add48701 Rat Prote	Aar24393 Sequence	Abo52933 Human spl
ABB57176	ABB78538	AA030407	AAR22380	ABR39650	AAB26153	ABB70499	ABP54340	ABP43151	ADD47283	AAW50193	AA002076	ADC87177	ABB65135	ABB62915	AAR12362	AAU28194	ADD48701	AAR24393	ABO52933
Ŋ	w	7	N	w	m	4	9	ഹ	7	~	4	7	4	4	~	4	7	7	9
1378	104	162	487	205	865	815	815	147	164	82	g Q	523	926	749	455	940	202	351	464
31.7	30.9	30.8	30.1	30.1	29.8	29.4	29.4	28.5	28.4	28.1	28.0	28.0	27.9	27.7	27.6	27.6	27.5	27.5	27.5
221	215.5	215	210	209.5	208	205	0	198.5	198	196	195.5	195.5	194.5	193	192.5	192.5	192	192	192
26	27	. 28	53	30	31	32	33	34	35	36	37	38	6 6	40	41	42	43	44	45

# ALIGNMENTS

Histidine proline rich glycoprotein; HPRG; rabbit; antiangiogenic; cytostatic; antiarteriosclerotic; antinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator. New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis. domain, region also 251. .296. /note= "Proline-rich domain" /note= "Histidine-proline-rich do /note= "Histidine-proline-rich do specifically claimed in Claim 1" Mazar AP; Rabbit histidine proline rich glycoprotein. Location/Qualifiers Claim 1; Page 12-13; 82pp; English. Plunkett ML, ABB79805 standard; protein; 526 AA. 14-FEB-2002; 2002WO-US004336. 14-FEB-2001; 2001US-0268370P. (first entry) Oryctolagus cuniculus. Donate F, Harris S, (ATTE-) ATTENUON LLC. WPI; 2002-666989/71. P-PSDB; ABN84911 WO200264621-A2. 25-NOV-2002 22-AUG-2002. ABB79805; Key Domain Domain RESULT 1 ABB79805 

The present sequence is the protein sequence of rabbit histidine proline rich glycoprotein (HPRG), a proteinaceous chelator that can be used to inhibit anglogenesis and treat cancer. Claimed anti-anglogenic

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CC doubties or peptides comprise: the histidine-proline-rich (H/P) donain (see ABB78806) of human HPRG; an H/P domain of rabbit HPRG (see ABB78017); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB7808. Also claimed are: chemically synthesised or recombinantly produced another; a diagnostically synthesised or recombinantly produced another; and agnostically synthesised or recombinantly produced anotypeptide, peptide or peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the H/P domain of specific for an epitope of HPRG that is present in the H/P domain of specific for an epitope of HPRG that is present in the H/P domain or away which inhibits the anti-angiogenic activity of HPRG or the domain. Or an antigen-binding fragment of the antibody a method for treating a subject having a disease or condition associated with undesired cell migration, or angiogenesis; a method of stimulating or inhibiting cell migration, call invasion, cell migration, invasion, cell migration, invasion, coll migration and peptide multimer; and subject, a method of stimulating or inhibiting angiogenesis in a subject; a method of stimulating or inhibiting caleavage product or its peptide or peptide multimer; and effinity ligand useful for binding molecule, comprising the protypeptide, peptide or peptide multimer; and affinity ligand useful for binding molecule, comprising the polypeptide, peptide or peptide multimer; and a method of isolating molecule, comprising or carrier; and a method of isolating HPRG-binding molecule, comprising or carrier; and a method of isolating HPRG-binding molecule, comprising or carrier; and a method of isolating HPRG-binding molecule, comprising or carrier; and a method of isolating site or receptor, from a condisease or condition associated with undesired cell migration, invasing and method secule or condition as o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The antibodies are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invasion, proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative diseases like Alzheimer's disease, barkinson's disease and amyotrophic lateral solenosis. The antibodies are stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoassays
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0; Gaps
                        100.0%; Score 697; DB 5; Length 526; 100.0%; Pred. No. 5.5e-51; ative 0; Mismatches 0; Indels (
                                                                                                                                  СНРРИСРРИСИРРИСРРИСИРРИСИРРИСРОРРЅН 101
                                                                                                                                               381 GHPPHGPPHGHPPHGPPHGHPHGHPHGHPHGFCDPPSHK 421
                                                   Matches 101; Conservative
                                      Local Similarity
Sequence 526 AA;
                         Query Match
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Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; cytostatic; antianteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiatrhitic; antiulcer; osteopathic; antitunour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator.
                                                                                                                   Human histidine proline rich glycoprotein.
                            ABB79804 standard; protein; 525 AA
                                                                                        25-NOV-2002 (first entry)
                                                           ABB79804;
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Homo sapiens

Sequence 525 AA;

mmunoassays

The present sequence is the protein sequence of human histidine proline rich glycoprotein (HPRG), a proteinaceous metal cheltor that can be used to inhibit angiogenis and treat cancer. Claimed anti-angiogenic to inhibit angiogenic coopidates the histidine-proline-rich (H/P) coopidates or peptides comprise: the histidine-proline-rich (H/P) coopidates or peptides comprise: the histidine-proline-rich (H/P) coopidates of the proliferation or endothelial tube formation in vitro or in vivo, or a pentapeptide having the generic sequence given in ABB79808. Coopidate multimers; a diagnostically protuced peptide multimers a diagnostically produced peptide multimer is diagnostically produced peptide composition. Comprising the diagnostically labeled antically peptide, peptide or peptide multimer; and antibody constitution or rabbit HPRG, and which binds to HPRG or to any of the domains in specific for an epitope of HPRG that is present in the H/P domain of specific for an epitope of HPRG that is present in the H/P domain in an antigen-binding fragment of the antibody; a method for the domains or an antigen-binding fragment of the antibody; a method for inhibiting coll invasion, or angiogenesis a method for treating a subject having a disease or condition associated with undesired cell migration, invasion, or angiogenesis is a method of stimulating or inhibiting and expression vector; transferded or beptide or peptide or peptide multimer; and efficitly ligand useful for binding to, or the peptide multimer; and affining to a cell, tissue or organ an angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its peptide in a biological sample; isolated collected or cells expressing the binding molecule, comprising the correction or angiogenesis in a subject and a method for insolating an ergopenial or cells expressing the binding molecule, cor respection or angiogenesing the binding molecule, comprising or cells expressing the binding steep or receptor, from a corrier; and expension or isolating and expension or angiog treating a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis, such as cancer, artheroscierosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative diseases like Alzheimer's disease. Parkinson's disease, and amyotrophic lateral sclerosis. The antibodies are stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various migration, diagnosing or treating diseases associated with undesired cell migratio invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis. New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for /note= "Histidine-proline-rich domain, region also specifically claimed in Claim 1" Mazar AP; /note= "Proline-rich domain" 350. .497 Location/Qualifiers Jonate F; Harris S, Plunkett ML, Claim 1; Page 11; 82pp; English. 14-FEB-2002; 2002WO-US004336. 14-FEB-2001; 2001US-0268370P. (ATTE-) ATTENUON LLC WPI; 2002-666989/71. P-PSDB; ABN84910 WO200264621-A2. 22-AUG-2002. Key Domain Domain  ő

Gaps

64;

Length 525;

45.1%; Score 314; DB 8; Length 52 ilarity 41.8%; Pred. No. 7.5e-19; Conservative 2; Mismatches 23; Indels

Local Similarity Les 64; Conserv

Query Match Best Loca Matches

Sequence 525 AA;

SXS

liver disorder.

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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful coff tracting liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of several molecules or compounds to identify a ligand which specifically binds a CDNA. A protein encoded by the CDNA is useful for high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the CDNA with several of molecules or compounds under conditions to allow specific protein which involves combining the protein encoded by the CDNA with several of molecules or compound, therefore identifying a ligand which specifically binds the protein. The compound, therefore identifying a ligand which specifically chinding perfect or compound, therefore identifying a ligand which specifically chinds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a
                                            æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                        330 ATFGTNGAQRHSHNNNSSDLHPHKHHSHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                                                         275 КРРГКРНGSRDHHHPHKP-----НЕНGРРРРРБВRDHSHGPPLPQGPPLLPMSCSSCQH
                                                                                                                                                                  Gaps
                                                                                     7 крр--рнд----ниридрридниридррр-----нднр-ридррр----
                                            64;
Length 525;
                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein expressed in a liver disorder #18.
Score 314; DB 5;
Pred. No. 7.5e-19;
2; Mismatches 23;
                                                                                                                                                                                                                                                                            390 HPHGHHPHGHHPHGHPHCHDFQDYGPCDPPPH 422
                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 62; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     ADE76897 standard; protein; 525 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-2001; 2001US-00919039.
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      45.1%;
41.8%;
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                                              Conservative
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                        1 Similarity
64; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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    Query Match
Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE76897;
                                                                                                                                                                                                                                                                                                                                                           RESULT 3
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The present sequence is the protein sequence of the histidine-proline-rich (H/P) domain of rabbit anti-angiogenic histidine proline rich palycoprotein (HFRG, see also ABR79805). Claimed anti-angiogenic polypeptides or peptides comprise: the H/P domain (see ABB79806) of human HPRG; an H/P domain of rabbit HPRG; a variant of these that is capable of tunbiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808. Also claimed are: chemically synthesised or trecombinantly produced peptide multimers a diagnostically or the rappended anti-angiogenic polypeptide, peptide or peptide multimer; a diagnostically useful HPRG-related composition, comprising the diagnostically labeled polypeptide, peptide or peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the H/P domain of human or rabbit HPRG, and which binds to HPRG or to any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
                                   275 КРРРКРНGSRDHHHPHKP-----НЕНGPPPPPDBRDHSHGPPLPQGPPLPQGPDLPMSCSSCQH 329
                                                                                                                  ззо атғатысадекенимызергірничыненедеріріненененененененененененененен зво
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histidine proline rich glycoprotein; HPGP; rabbit; antiangiogenic; cytostatic; antiarteriosclerotic; antinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator.
                                                                            67
                                                                              -----КНЪ,-----РИСРРРИСИРР-----КИРРРИСИРРИС
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rabbit histidine proline rich glycoprotein His/Pro-rich domain.
7 крр--рнд----ниридррридинридрр------ндир-ридррр
                                                                                                                                                                                              390 HPHGHHPHGHHPHGHPHGHPHGHPHGHPFQDYGPCDPPPH 422
                                                                                                                                                                   68 РРНGНРРНGРРРНGНРРНGНGFHDHGPCDPPSH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plunkett ML, Mazar AP;
                                                                                                                                                                                                                                                                                                                    ABB79807 standard; protein; 148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 13; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2002; 2002WO-US004336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2001; 2001US-0268370P.
                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donate F, Harris S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ATTE-) ATTENTION LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-666989/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABN84910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200264621-A2.
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of the domains in a way which inhibits the anti-angiogenic activity of HPRG or the domain, or an antigen-binding fragment of the antibody; a method for inhibiting cell migration, cell proliferation or angiogenesis, a method for treating a subject having a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis; a method of simulating or inhibiting angiogenesis in a subject; a method of detecting the presence of HPRG or its cleavage product or its peptide, peptide or peptide multimer; an expression vector; transformed or transfected cells; a method of providing to a cell, tissue or organ an angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its pentapeptide, or the peptide multimer; an affinity ligand useful for binding to, or isolating, HPRG-binding molecule, comprising the polypeptide, peptide or peptide multimer, immobilised to a solid support or carrier; and a method of isolating HPRG-binding site or isolating or enriching or cells expressing HPRG-binding site or isolating or treating a method of compositions and methods are useful in diagnosing or treating a disease or or condition associated with undesired cell migration, invasion, consistent and methods are useful in diagnosing or treating disheric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferation, or angiogenesis, such as cancer, atheroscierosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in tracting neurodegenerative diseases like Alzheimer's or Parkinson's disease. The antibodies are stimulators of angiogenesis and are useful for promoting neurodescenting neovascularization in pertinent disease states, and in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoassays
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24; Indels 19; Score 280.5; DB 5; Length 148; Pred. No. 1.7e-16; 1; Mismatches 24; Indels 19; 40.2%; 51.6%; Query Match
Best Local Similarity 51...
And 47; Conservative Sequence 148 AA; g ò

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Gaps

Human histidine proline rich glycoprotein His/Pro-rich domain. ABB79806; 

ABB79806 standard; protein; 148 AA. 25-NOV-2002 (first entry)

cytostatic; antiarterioscierotic; antiinfiammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian. Histidine proline rich glycoprotein; HPRG; human; antiangiogenic;

Homo sapiens.

WO200264621-A2. 22-AUG-2002. 14-FEB-2002; 2002WO-US004336.

14-FEB-2001; 2001US-0268370P.

(ATTE-) ATTENUON LLC.

Mazar AP; Donate F, Harris S, Plunkett ML,

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The present sequence is the protein sequence of the histidine-proline-
cc rich (HPMP) domain of human anti-anglogenic histidine proline rich
dyproprides or peptides comprises the HPM domain of human HPMP,
and of rabbit HPMPG, see ABB12345); a variant of these that is capable
cc domain of rabbit HPMPG (see ABB12345); a variant of these that is capable
cc dimibiting angiogenesis, endothelial cell proliferation or endothelial
cc finibiting angiogenesis, endothelial cell proliferation or endothelial
cc funbe formation in viero or in vivo; or a pentapeptide having the generic
cc the formation in ABB19808. Also claimed are: chemically synthesised or
recombinantly produced anti-angiogenic polypeptide, peptide or peptide
cc recombinantly labeled anti-angiogenic polypeptide, peptide or peptide
cmultimer; an antibody specific for an epitope of HPMP or peptide
cc arrier; an antibody specific for an epitope of HPMP or peptide
cc the Gomain of human or rabbit HPMC, and which binds to HPMC or to any
cc the Gomain of human or rabbit HPMC, and which binds to HPMC or to any
cc the Gomain of human or rabbit HPMC, and which binds to HPMC or to any
cc the Gomain of human or antiger-binding fragment of the antibody; a
method for inhibiting call migration, cell invasion, cell proliferation
cc transfected for inhibiting angiogenesis; a method of transfected cells angiogenesis; a method of angiogenesis, an authody
cc angiogenesis, or for inducing apoptosis; a method of angiogenesis and product or its peptide
cc stimulating or inhibition angiogenesis; a method of
cc angiogenesis. Inhibition and product or its peptide
cc the presence of HPMC or its cleavage product or its peptide
cc the prince or peptide multimer; an expression or calls expressing
cc the binding molecule, comprising the polypeptide, polypeptide, peptide or spelide or spelide sequence of the polypeptide
cc binding molecule, comprising the polypeptide, peptide or or peptide
compositions and method of sequence or peptide
cc sompositions are useful in diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative diseases like Alzheimer's or Parkinson's disease. The antibodies are
                                                                                      New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or anglogenesis, e.g. cancer, atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various
                                                                                   New histidine-proline rich glycoprotein (HPRG)
                                                                                                                                                                                                  Claim 1; Page 13; 82pp; English.
WPI; 2002-666989/71.
                             P-PSDB; ABN84910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 148 AA;
                                                                                                                 diagnosing or
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2 РНКННЅНЕОНРНСНИРНА------НН-----РНЕНDТНКОНРНСНИР 42 Gaps 40.2%; Score 280.5; DB 5; Length 148; Indels 24; Pred. No. 1.7e-16; Mismatches 24 40.2. 51.6%; Pre-47; Conservative Local Similarity Query Match Matches

70 НGНРРНGРРРНGНРРНGНGFUDPPSH 100 43 нанирнанирнанирнскоруарсоррын 73 ઠે

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ABG09949 standard; protein; 491 AA. RESULT 6
ABG09949
ID ABG0
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AC ABG0
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ABG09949;

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entry)

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                         Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                     Rat Protein L17318, SEQ ID NO 10875
                                 ADD45442 standard; protein; 296
                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-268312/26.
GENBANK; L17318.
                                                                                                                                                                                                                                                      Rattus norvegicus.
                                                                                                                                                                                                                                                                                          WO2003016475-A2.
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Best Local Simi
Matches 63;
                                                                                                               29-JAN-2004
                                                                                                                                                                                                                                                                                                                                  27-FEB-2003
                                                                         ADD45442;
                ADD45442
                                     The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity responsible for genetic disorders or other traits to assess blodiversity and canno acid sequences. Abg00010-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the will be printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 зрранснионкню ренионкернятанно ненежеррансино ненежноствой
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 НЕРРР-----НЭННРНС-----РРРНОНГОРОРИСИРРИСИРРИСИРРИЧ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.9%; Score 264.5; DB 4; Length 491;
.larity 41.8%; Pred. No. 1e-14;
Conservative 2; Mismatches 35; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 40308; 103pp; English.
                                     Novel human diagnostic protein #9940.
                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGFHDHGPCDPPSH 100
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGHHQHRP--PPAH
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Matches 56; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73.
N-PSDB; AAS74136.
                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 491 AA;
                                                                                                                                                                          WO200175067-A2.
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biodiversity.
  13-FEB-2002
                                                                                                                                                                                                                11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
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Costigan M;

Befort K,

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a chart is differentially expressed in returnal tissue of a first animal that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in natural subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating to pain and a pharmaceutical composition compressing the one or more of the polypeptides given in the compound that in an animal of one or more of the polypeptides given in the compound that it is useful for preparing a medicament for treating pain and spared nerve injury (SNI) in an animal (e.g. spinal segmental nerve injury (SNI) in an animal (e.g. spinal segmental nerve injury (SNI) in an animal (e.g. spinal nerve injury (SNI) in an animal (e.g. spinal composition which is differentially expressed during pain. Note: the specification, but was obtained in electronic form directly from WIPO at specification, but was obtained in electronic form directly from WIPO at the polyment in the composition of the specification, but was obtained in electronic form directly from WIPO at
Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 296 AA;
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---GPPPHG----HHPHGPPPHGHP-- 34

VNI IHRPPPHG---HHPH--

27; Indels 73; Gaps

37.2%; Score 259.5; DB 7; Length 296; llarity 38.4%; Pred. No. 1.7e-14; Conservative 1; Mismatches 27; Indels 73;

Similarity

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, clarivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates the activity in an animal of one or more of the polynpetides given in the activity in an animal of compound or more of the polynpetides given in the activity in an animal or identifying a compound useful in the activity in an animal or identifying a compound useful in the
141 PPQPGSPQGPPPPGGPQQRPPQGPPPQGGPQRPPQPGSPQGPPPPGGPQQRAPQGPPPG 200
                                                           71
                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                         -----PHGPPP----PHGPPHGPPHGHP-----PHGPPPHGHP----PHGPPPHG
                                                                                                                                                                    201 GPORPPOPGSPOGPPPGGPQORPPOGPPOG-----GPORPP 238
                                                                                                                                    86
                                                                                                                                  72 HP-----PHGP-----PPHGHPPHGHGFHDHGPCDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Costigan M;
                                                                                                                                                                                                                                                                                                                                                                              Rat Protein L17318, SEQ ID NO 2965.
                                                                                                                                                                                                                                                                 ADE57105 standard; protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page, 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-268312/26
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34
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the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                71
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                     VNR PER PPQHGGNIHIH PHIPPPPAAGPQR PPQPGSPQGPPPGGPQQRPPQGPPPQGGPQR
                                                                                                                                                                                                35 -----РНGРР-----РНGРРНGРРНG-----РНGРРНGНР-----
                                                                                                                                            ---- СБРРНС---- ННРНСРРНСНР---
                                                                                                                   Gaps
                                                                                                                  73;
                                                                                          Length 296;
                                                                                         Score 259.5; DB 7; Length
Pred. No. 1.7e-14;
1; Mismatches 27; Indels
                                                                                                                                                                                                                                                                            201 GPORPPOPGSPOGPPPGGPOORPPOGPPPOG-----GPORPP 238
                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                     ----PPHGHPPHGHGFHDHGPCDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                         Rat Protein AAA42064, SEQ ID NO 12934.
                                                                                                                                                                                                                                                                                                                                            ADD47240 standard; protein; 274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 1017pp; English.
                                                                                                                                              2 VNIIHRPPPHG---HHPH---
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                                                                                       37.2%;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                   63; Conservative
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-268312/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BENBANK; AAA42064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003016475-A2.
                                                                 Sequence 296 AA;
                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                      ADD47240;
                                                                                                                                                                                                                                                   72
                                                                                          Query Match
Best Local &
                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                               ADD47240
                                                                                                                                                                                                                                                                                                                   RESULT
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The invention discloses a composition comprising two or more isolated rat derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an open that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence subjected to pain, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially

pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of

us-10-074-225a-6.rag

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expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymeldes, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polymeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polymeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain and appared nerve injury (cumy), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form mark of the printed specification, but was obtained in electronic form directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
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Sequence 274 AA;

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219
                                                                                                                     104 PPPGGPQQRPQGPPPPGGPQGPPQGPQGPQGPPPGGPQGPPPPGGPPPPGGPQ 163
                                                                                                                                                                              54 -- РИСРРРИС---- НРРИСРРИСИР---РИСРРИСИРРИСИСИТИВИСР------СОР 97
                                                                                                                                                                                                             164 QGPQGPPPGGPQQSPPQGPPPPGGPQQPPQGPPPPGGPQQGR----QGPPPPGGPQQDP
                                                                                            29; Indels 34; Gaps
Query Match 35.3%; Score 246; DB 7; Length 274; Best Local Similarity 47.1%; Pred. No. 2.2e-13; Matches 57; Conservative 1; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                220 P 220
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Rat Protein AAA42064, SEQ ID NO 14412. ADD48703 standard; protein; 274 AA. 29-JAN-2004 (first entry) ADD48703; RESULT 10 ADD48703 

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

Rattus norvegicus.

WO2003016475-A2. 27-FEB-2003 14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

14-AUG-2002; 2002WO-US025765

(GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.

Costigan M; Befort K, Woolf C, D'urso D,

WPI; 2003-268312/26 GENBANK; AAA42064. New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector, a method for identifying a nucleotide sequence which is differentially respected in a manimal subjected to pain and a fixt to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in meuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that and a pharmaceutical composition compound useful in treating method for identifying a compound or feature that regulates the activity of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain (e.g. spinal segmental nerve injury (Cung), chronic construction composition compising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Cung), chronic construction continity (CCI) and sparad nerve injury (KNI) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: the specification, but was obtained in electronic form directly from MIPO at the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from wipo int/pub/published_pot_energe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 <u>gGPOGPPPPGGPQQSPPQGPPGGPQGPQGPPGBPPGGPQQGR----QGPPPPGGPQQDP</u> 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 -- PHGPPPHG----HPPHGPPPHGHP---PHGPPPHGHPPHGHGFHDHGP-----CDP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 35.3%; Score 246; DB 7; Length 274; Local Similarity 47.1%; Pred. No. 2.2e-13; Local Similarity 47.1%; Pred. No. 2.2e-13; Local Similarity 1; Mismatches 29; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 274 AA;
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AAR04119 standard; protein; 274 AA. ORF2 of Enod2b genomic clone. (revised)
(revised)
(first entry) 24-OCT-2003 25-MAR-2003 05-JUN-1990 AAR04119; RESULT 11 AAR04119

(L) Merr. cv. Williams Glycine max; 03-JAN-1990, EP349338-A. 

ORF2; Enod2; soybean; root nodule; nodulin 75.

88US-00214297. 88US-00214297. 01-JUL-1988; 01-JUL-1988;

(LUBR ) LUBRIZOL GENETICS INC

11;

Length 309; Indels

N-PSDB; AAQ03097

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The invention discloses a composition comprising two or more isolated rat or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynuclectide sequence subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence the expression of a polynuclectide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the
ORFI actually encodes the protein, N-75. The polypeptide encoded by ORFI is proline-rich and as such, prone to aberrent behaviour during SDS PAGE analysis as was found with the actual translation product. Also, a hybrid translation prod. contained no methionine residues; ORFI has only one whereas ORF2 has about 20 met codons. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                   95 КРРРЕУОРРИЕКРРИ----ЕМРРРЕНОРРИЕКРРЕНОРРИЕКРРЕУЕРБИЕКРРЕУОР 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                         Human, pain, neuronal tissue, gene therapy, spinal segmental nerve injury, chronic constriction injury, CCI, spared nerve injury, SNI, Chung.
                                                                                                                                                                                                                                                                                                                                                                                                     64 PH-GPPPHGHPPH-GPPPHGHPPHGHGFHDHGPC--DPPSHK 101
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                                                                                                                                                                                                             33.5%; Score 233.5; DB 2;
48.0%; Pred. No. 2.7e-12;
tive 3; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Protein PIHUB6, SEQ ID NO 11408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD45740 standard; protein; 331 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Χ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                      | Similarity
49; Conserv
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(FARB ) BAYER AG
                                                                                                                                                                   Sequence 309 AA;
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Best Local S:
Matches 49,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD45740;
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                                                                                                                                                                                                                                                          Two open reading frames are present in the cDNA of the Enod2b genomic clone, ORF1 and ORF2 (AAR04118 and AAR04119 resp.) but it is thought that ORF1 actually encodes the protein, N-75. The polypeptide encoded by ORF1 is proline-rich and as such, prome to aberrent behaviour during SDS PAGE analysis as was found with the actual translation product. Also, a hybrid translation prod. contained no methionine residues; ORF1 has only one whereas ORF2 has about 20 met codons. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                             EnoD2 gene regulatory region - used for early expression of structural gene in developing root nodule of soybean plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EnoD2 gene regulatory region - used for early expression of structural
gene in developing root nodule of soybean plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 КРРРЕУОРРНЕКРРН----ЕNPPPEHQPPHEKPPEHQPPHEKPPPEYEPPEYQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 КРРРИСИНРИСРРРИСИНРИСРРИСИРРИСРРИСИР-СРРИСИРРИ-СРРИСИР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PH-GPPPHGHPPH-GPPPHGHPPHGHGFHDHGPC--DPPSHK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           РНЕКРРРЕТОРРНЕКРРРЕТОРРНЕКРРРЕНОРРНЕКРРЕНО 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 233.5; DB 2;
48.0%; Pred. No. 2.5e-12;
iive 3; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORF1; Enod2; soybean; root nodule; nodulin 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                  Disclosure; Page 14-16; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cv. Williams
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                                Franssen H, Bisseling AH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 48.0
nes 49; Conservative
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                                                                            WPI; 1990-009296/02
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24-OCT-2003 25-MAR-2003 05-JUN-1990

AAR04116;

RESULT 12

64

g ö 셤 Glycine max;

01-JUL-1988; 01-JUL-1988;

03-JAN-1990 EP349338-A

Sequence 274 AA;

Query Match Matches Two open reading frames are present in the cDNA of the Bnod2a genomic clone, ORF1 and ORF2 (AAR04116 and AAR04117 resp.) but it is thought that

Disclosure, Page 12-13; 18pp; English.

N-PSDB; AAQ03098

Franssen H,

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polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                 8X9293335555555588
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Sequence 331 AA;

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                                                                                                   101 PPOGGNOPOGEPPPPGKPQGPPPQGGNKPQGPPPPGKPQGPPPQGDKSQSPRSPPGKPQG 160
                                                                    8 ЭБИСИНРИСРРИНИНОВРЕННИВ СИРРИСРРИНЕРВИСРЕНСИ 56
                                                                                                                                                                   PPPQGGNQPQGPPPPPGKPQGPPQQGGNRPQGPPPGKPQGPPPQGDKSRSPQSPP 216
                                      25; Gaps
                                                                                                                                        PPPH-GHPPHGPPP------HGHPPHGPPPHGHP--PHGHGFHDHGPCDPP 98
      Length 331;
                                    Indels
   Score 233.5; DB 7;
Pred. No. 2.9e-12;
4; Mismatches 38;
      33.5%;
Soury Match
Best Local Similarity 42.29
Matches 49, Conservative
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ABO52997 standard; protein; 424 AA. ABO52997; RESULT 14 

09-OCT-2003 (first entry)

Human spliceosome associated protein (SAP) #24.

Human, SAP; spliceosome associated protein; ribonucleoprotein; RNP complex; RNA affinity substrate; RNP assembly sequence; spliceosomal complex; hnRNP complex; mRNA export complex; mRNA localisation complex; RAP editing complex; intron complex; H complex; telomerase complex; fragile X protein complex; reverse transcriptase complex; gene splicing complex.

Homo sapiens

US2003068803-A1.

10-APR-2003

14-JAN-2002; 2002US-00047991.

12-JAN-2001; 2001US-0261521P.

(REED/) REED R. (ZHOU/) ZHOU Z.

Zhou Z; Reed R, WPI; 2003-540885/51.

Isolating ribonucleoprotein complex, by contacting RNA affinity substrate having ribonucleoprotein assembly sequence and affinity tag, with protein mixture, subjecting complex formed to chromatography, affinity selection.

Claim 24; Page; 39pp; English.

The invention relates to forming (MI) an isolated ribonucleoprotein (RNP) complex (C), involves contacting an RNA affinity substrate (S) comprising an RNP assembly sequence (AS) and an affinity tag, with a protein mixture

(GEST ) GENSET SA

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to permit formation of (C) on AS, subjecting (C) to chromatographic separation, and subjecting (C) to affinity selection, where the affinity casparation, and subjecting (C) to affinity selection, where the affinity maltose binding protein binds to an affinity matrix. Also included are an isolated spliceosome preparation (isolated by (MI)), a RNA comprising can RNP complex binding site and at least one phage cost protein crooping they and least one phage cost protein complex binding site and at least one phage cost protein complexed by (MI) a subject having a disorder associated with abnormal RNP complexes (by cobtaining a sample of calls from a subject, purifying RNP complexes (by the cells of the subject by (MI), determining the presence in the complex bin the subject. (MI) is useful for forming an isolated RNP complex, an hurby complex, an mRNA export complex, or an H complex. (complex selected from a spliceosomal complex, or an H complex. (MI) is useful for treating a subject having a disorder associated with abnormal RNP complexes. (MI) is useful for treating a subject having a complex, an an end and an end of the subject is useful for treating a subject having a disorder associated with abnormal RNP complexes. (MI) is useful for treating a subject having a complex, an everse transcriptuse complex, a fragile X complex. The present sequence represents a known human spliceosome complex. The present sequence represents a known human spliceosome complex. The present sequence represents a known human spliceosome complex complex. The present sequence represents a known human spliceosome complex. The present sequence represents a known human spliceosome complexed the sequence is not shown in the sneed for the invention. Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 РGHGHSHPHPFPPPGGMPHPGMSQMQLAНHGPHGLGHPHAGPPGSGGQPPPRPPPGMPHPG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; forensic analysis; chromosome marker; organelle-specific marker; novel-related disorder; neurological disorder; gene therapy; nootropic; neuroprotective; salivary proline-rich protein; Saprip.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The prsent sequence is not shown in the specification but was obtained from Genbank or Swissprot using the information provided in table 1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PHG-HHPHGPPP--HGHPPHG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 233.5; DB (
Pred. No. 3.5e-12, 
3; Mismatches 25
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14-DEC-2001; 2001US-0340465P.
18-APR-2002; 2002US-0373947P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%;
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nes 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 424 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2003.
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New isolated polynucleotides and polypeptides useful as reagents in forensic analyses, as chromosome markers, as tissue/cell/organellespecific markers, in producing expression vectors, or in screening and diagnostic assays.
       Bejanin S, Tanaka H;
                         WPI; 2003-505202/47.
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Disclosure; Page 166; 242pp; English.

The invention relates to human novel polynucleotide and polypeptide sequences useful as reagents in forensic analyses, as chromosome markers, as tissue/cell/organelle-ppecific markers, in producing expression vectors, or in screening and diagnostic assays. The invention is used as reagents in screening and diagnostic assays for abnormal novel expression and/or biological activity, and in screening compounds that may be used in the treatment of novel-related disorders, e.g. neurological disorders. The novel gene is also used in gene therapy. The present sequence is human cp3 salivary proline-rich protein splice variant (Saprip) fragment of the invention

Sequence 192 AA;

Gaps Score 231.5; DB 6; Length 192; Pred. No. 2.7e-12; 3; Mismatches 40; Indels 15; Query Match
Best Local Similarity 44.8%;
Matches 47; Conservative 6 рендиристринундернундернундернундернундернундернундернундер 57 

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Search completed: September 23, 2004, 22:50:05 Job time: 71.9558 secs

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September 23, 2004, 22:33:30; Search time 20.2811 Seconds (without alignments) 479.034 Million cell updates/sec
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697
1 SVNIIHRPPPHGHHPHGPPP.........HPPHGHGFHDHGPCDPPSHK 101
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                         283366 seqs, 96191526 residues
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                    Copyright
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Perfect score:
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Total number of hits satisfying chosen parameters: length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Searched:

283366

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	stidine		Ħ			acidic proline-ric	proline-rich prote	rich	Ine-rich	rich	Enod2	salivary proline-r	extensin - soybean	extensin precursor	glycine/proline-ri	nodulin precursor	spliceosome-associ	zinc finger protei	ar	proline-rich prote	line-rich	_	proline-rich prote	proline-rich prote	14	-rich	ine-rich pro	le-specif	proline-rich prote
ов гр	1 KGHUGH		2 B48013	D3835	B3906	PIRT	C291	A2426				PIHUB		T1086			A5496		PIHUP		B3629	PIHUS	A3629	S1088	T3017	D4075	E291	S1196	S2373
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rhodopsin - Allote hydroxyproline-ric	nodulin - alfalfa proline-rich prote	nypounctical proce nodulation protein	proline-rich prote	basic proline-rich rhodopsin - northe	proline-rich prote hypothetical prote	proline-rich prote	proline-rich prole hypothetical prote	carboxypeptidase C
S60755 S06733	S04554 A42817	S10101	128//U A48013	JH0481 S14332	B29149 T49482	A30496	S22373 T32402	T43236
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210 210	209	206.5	204.5	202	199.5	198	197.5	197.5
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### ALIGNMENTS

		- human	
		precursor	
RESULT 1	KGHUGH	histidine-rich glycoprotein	N:Alternate names: HRG

		C,Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 16-Jun	·
N'STREETINGS TRAINED	C;Species: Homo sapiens (man)	C,Date: 04-Dec-1986 #sequence	C; Accession: A01287; S29669

Ricoide, T.; Foster, D.; Yoshitake, S.; Davie, E.W.
Biochemistry 25, 2220-2225, 1986
Biochemistry 25, 2220-2225, 1986
A; Fittle: Anino acid sequence of human histidine-rich glycoprotein derived from the nucle A; Fittle: Anino acid sequence of human histidine-rich glycoprotein derived from the nucle A; Fittle: Anino acid sequence of human histidine in A; Rocession: A01287
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-525 < KOI>
A; Cross-references: GB:AB005803; NID:g2280513; PIDN:BAA21613.1; PID:g2280514
A; RiHennis, B.; Havelaar, A.; Kluft, C.
Submitted to the EMBL Data Library, October 1991
A; Description: PCR detection of a dinucleotide repeat in the human histidine-rich glycop
A; Reference number: S29669

A; Accession: 529669
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Colecule type: DNA
A; Residues: 214-247
A; Coomment: Dreliminary
A; Coomment: Although its physiological function is not yet known, HRG does bind heme, dy:
C; Comment: Although its physiological function is not yet known, HRG does bind heme, dy:
din, and the lysine-binding site of plasminogen. On the basis of its homology with HWW }
lood coagulation cascade.
C; Comment: The amino half of this protein is homologous to the first two cystatin-like ould not have inhibitory activity.
C; Comment: In addition to having a high histidine and proline content, this protein has

Aymap position: 327-327
CySuperfamily: histidine-rich glycoprotein; cystatin homology
CySuperfamily: histidine-rich glycoprotein; cystatin homology
CySuperfamily: histidine-rich glycoprotein binding; tandem repeat
F;1-18/Domain: signal sequence #status predicted <813>
F;19-525/Product: histidine-rich glycoprotein #status predicted <MAT>
F;19-131/Domain: cystatin homology <CY1>
F;10-246/Domain: cystatin homology <CY2>
F;10-246/Domain: proline-rich
F;348-437/Region: histidine-rich
F;351-25,344,345/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;78-89;105-126,218-241/Disulfide bonds: #status predicted C;Genetics: A;Gene: GDB:HRG A;Cross-references: GDB:120055; CMIM:142640 e-rich' region.

ch 45.1%; Score 314; DB 1; Length 525; 1 Similarity 41.8%; Pred. No. 1.1e-16; 64; Conservative 2; Mismatches 23; Indels Query Match Best Local Similarity Matches 64; Conserv

40 Gaps 64;

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2 VNIIHRPPPHG---HHPH-
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Best Local Similarity 38.4
Matches 63; Conservative
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Mistidine-rich glycoprotein - bovine (fragments)
Mistidine-rich glycoprotein - bovine (fragments)
Mistidine-rich glycoprotein - bovine (actte)
C;Species: Bos primigenius taurus (catte)
C;Species: Bos primigenius taurus (catte)
C;Species: Bos primigenius taurus (32648)
C;Accession: 335687, J02196, A60488
R;Sorensen, C.B.; Krogh-Pedersen, H.; Petersen, T.E.
R;Sorensen, C.B.; Krogh-Pedersen, H.; Petersen, T.E.
A;Title: Determination of the disulphide bridge arrangement of bovine histidine-rich gly
A;Reference number: S35687; MUID:93351678; PMID:8348977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein

A; Residues: 1-25,56-52,57-57,82-88,95-119,146-173,175-206;210-309;313-445 <8OR>
A; Residues: 1-25,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,56-52,
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Kesidues: 1-23;35-54,'VK',57-101,'R';'TVGEYTEG',116,'N',118,'R',120-136;137-145;150-20
A;Experimental source: plasma
R;Vestergaard, A.B.; Andersen, H.F.; Magnusson, S.; Halkier, T.
Thromb. Res. 60, 385-396, 1990
A;Title: Histidine-rich glycoprotein inhibits contact activation of blood coagulation.
A;Reference number: A60488; MUID:91196010; PMID:2084959
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A;Residues: 1-6,'X',8-15 <VES>
C;Comment: This protein is a single-chained plasma protein which participates in transgl
C;Superfamily: histidine-rich glycoprotein; cystatin homology
C;Keywords: glycoprotein; plasma
F;2-113/Domain: cystatin homology <CY1>
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F;7-424,60-71,87-108,165-346,180-203,258-288/Disulfide bonds: #status experimental
F;74,107,164,266/Binding site: carbohydrate (Asn) (covalent) #status experimental
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:|| ||| ||| || ||| || 275 KPPFKPHGSRDHHHPHKP-----HEHGPPPPDERDHSHGPPLPAGPPLLPMSCSSCQH 329
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                                                                                                                                                                                                             330 ATFGTNGAQRHSHNNNSSDLHPHKHISHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGH
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                                                                                                                                 ---PHGPPPHGHPP-----HGPPHGHPHGP 67
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42.4%; Pred. No. 8.7e-13;
iive 4; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                         390 НРИСКИРНСКИРНСКИРНСКОРГОРГОРРРИ 422
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Best Local Similarity 42.4
Matches 53; Conservative
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PPPHR 352
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proline-rich proteoglycan 2 precursor, parotid - rat C;Species: Rattus norvegicus (Norway rat) C;Date: O2-Jun.1995 #sequence\_revision 02-Jun-1995 #text\_change 20-Aug-1999 C;Accession: B48013

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R;Castle, A.M.; Castle, J.D.

Biol. Chem. 268, 20490-20496, 1993

A;Title: overlander 268, 20490-20496, 1993

A;Title: overlander 268, 20490-20496, 1993

A;Title: overlander 268, 20490-20496, 1993

A;Reference number: A48013, MUID:93388626; PMID:8376404

A;Accession: B48013

A;Accession: B48013

A;Accession: B48013

A;Accession: B48013

A;Accession: B48013

A;Accession: B48013

C;Superiminary

A;Accession: B48013

A;Accession
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 12-Apr-1995
C;Accession: D38355
R;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
A;Title: Basic proline-rich proteins from human parotid saliva: relationships of the cov
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: B39066
R;Lin, H.H.; Ann, D.K.
Genomics 10, 102-113, 1991
A;Title: Molecular characterization of rat multigene family encoding proline-rich protein A;Reference number: A39066; MUID:91257817; PMID:2045095
A;Accession: B39066
A;Accession: Byee: DNA
A;Residues: 1-278 < LIN>
A;Residues: 1-278 < LIN>
A;Cross-references: GB;M36414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 PPQPGSPQGPPPPGGPQQRPPQGPPPQGGPQRPPQPGSPQGPPPPGGPQQRAPQGPPPQG 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 -----РНGРРР-----RHPPHGPPPHGHP-----РНGРРНGHP----РНGРРНG
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Pred. No. 7.3e-13;
1; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 HP-----PHGP-----PPHGHPPHGHGFHDHGPCDPP
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A, Status: preliminary
A, Molecule type: protein
C, Superfamily: proline-rich protein
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C,Accession: A28996
R;Ann, D.K.; Smith, K.; Carlson, D.M.
Biol. Chem. 263, 10887-10893, 1988
A;Title: Molecular evolution of the mouse proline-rich protein multigene family. Insert:
A;Reference number: A28996; MUID:88273214; PMID:2839509
A;Accession: A28996
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C;Genetics:
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RjAnn, D.K.; Carlson, D.M.
J. Biol. Chem. 260, 15863-15872, 1985
J. Biol. The structure and organization of a proline-rich protein gene of a A;Title: The structure A92508; MUID:86059475; PMID:2999141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proline-rich protein M14 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           proline-rich protein MP2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 RPPSGFQPRPPVNGSQQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPQ
                                                                                                         33 RPPPSGFQPRPPVNGSQQGPPPPGGPQPRPPQGPQPRPPQGPQPRPPQ
                                                                 ---BHGAH----HBBHGB----HBBHGBBBHG----HBBHGBHBHG----
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Kyeywords: sallan
F;1-15,Domain: signal sequence #status predicted <81G>
F;1-15,Domain: signal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 240;
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                      Indels
Pred. No. 5.3e-12;
0; Mismatches 34;
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llarity 43.6%; Pred. No. 5.6e-12;
Conservative 0; Mismatches 34;
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C; Superfamily: proline-rich protein
  43.68;
                                                                                                                                                                                                                                                                                                            153 PAGPQPRPPQGPP 165
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                                                                                                                                                                                                                                                            87 -HGFHDHGPCDPP 98
Local Similarity 43.6
nes 58; Conservative
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Matches 58; Conserv
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A; Residues: 1-317 <ANN>
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Local Sim-
58;
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     Best Loc
Matches
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NyAlternate names: PRP
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C;Accession: A03296
R;Ziemer, M.A.; Swain, W.F.; Rutter, W.J.; Clements, S.; Ann, D.K.; Carlson, D.M.
A;Title: Nucleotide sequence analysis of a proline-rich protein cDNA and peptide homolog
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R;Clements, S.; Mehansho, H.; Carlson, D.M.
J. Biol. Chem. 260, 13471-13477, 1985

A;Title: Novel multigene families encoding highly repetitive peptide sequences. Sequence A;Concents: Clone pumP40

A;Accession: C29149
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                                                                                                                                                                                                                                                                                  52 HP---PHGPPPHGHP---PHGPPPHGHP---PHGPPHG----HPPHG----HGFHDHGPC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 20-Aug-1999
                                                                                                                                                                                        52 PPPKGGPQQRPPQGPPPGGPQQKPQGPPPGGPQQRPPQGPPPPGGPQQGPPQGPPPG
                                                                                                                                               8 РРРИС---- НИРИСРРИС---НИРИСРРИС---- ВИРИСРРИСРРИСРРИСРРИСР
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*Residues: 1-27 < CLES

A; Cross-references: GB: M11902; NID: 9200544; PIDN: AAA40003.1; PID: 9200545

C; Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Nucleotide sequence analysis of a proline-rich protein cDNA and A,Reference number: A03296; MUID:84289443; PMID:6547951
A,Accession: A03296
A,Molecule type: mENA
A,Residues: 1-206 <21EA
A,Grestences: GB:K02247; MID:9206395; PIDN:AAA41949:1; PID:9206396
C,Comment: This protein contains six 18- to 19-residue repeats.
C,Comment: This protein may protect teeth by binding to tannins.
C,Superfamily: proline-rich protein
C,Reywords: duplication; parotid Gland; saliva; tandem repeat
F,11-13/Domain: signal sequence #status predicted <81G>
F,14-206/Product: acidic proline-rich protein #status predicted <MAT>
F,80-189/Region: 18-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                  32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 РОССРООКРРОРСКРОСРРОС-СРОСРРОРСИРОСРРОССИООКРРОР
                                                    Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                               32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.5%; Score 247.5; DB 1; Best Local Similarity 48.2%; Pred. No. 4.1e-12; Matches 53; Conservative 4; Mismatches 30;
                                                  Score 248; DB 2;
Pred. No. 4.9e-12;
1; Mismatches 32;
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     C; Superfamily: proline-rich protein
                                                    35.6%;
llarity 47.2%;
Conservative
                                                  Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     172 GPP 174
                                                                                                                                                                                                                                                                                                                                       96 DPP 98
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Length 227;

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DB

Score 246.5;

Query Match

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A; Accession: B40750
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Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Misseria (house)

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                                                                                                                                                                                                                                                                                                                            93 ĞРРРФССРОРКРРФСРРРФССРОРКРРФСРРРФСРРФРССРОРКРРФСРРФСРООКРРФСР
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                                                                                                     RPPPSGSQPRPPVNGSQQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQ 92
                                                                                                                                                                                                                            ---HPPHG--- 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Condin Bnod2 - Sesbania rostrata
Cispecies: S2140
Ride Bruijn, P.J.
Submitted to the BMBL Data Library, November 1991
Aireterence number: S2140
Airetesion: Cispecies: Cispecies:
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RPPPHGHHP----HGPPPHG----НИРНGPPPHG----НРРНGPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 РРРИСИРРИСРРИСИРРИСИРРИСИРРИСИСИСО--РРЅНК 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 240;
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41.1%; Pred. No. 4.4e-11;
ive 10; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proline-rich protein MP3 - mouse (fragment)
                                                                                                                                                                                                                      GPPPHG----HPPHGPPHG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 PGGPQPRPPQGPP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                             87 -HGFHDHGPCDPP 98
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Best Local Similarity 41.1
Matches 44; Conservative
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tes 58; Conserv
                                                                                                     33
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Niconstrains peptide 18-10 periods -2 (peptide 18-9); peptide PF p
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glycime/proline-rich protein - Arabidopsis thaliana
NyAlternate names: protein K10A8_130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51469
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Me'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.Alternate names: cell wall protein; hydroxyproline-rich glycoprotein C;Species: Phaseolus vulgaris (kidney bean)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
R;Accession: T10863; E3935
Blant Physiol. 109, 41-52, 1995
A;Title: Stress activation of a bean hydroxyproline-rich glycoprotein promoter is super.
A;Reference number: Z17192; MUID:96061709; PMID:7480331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-580 <WRS.
A;Residues: 1-580 <WRS.
A;Cresidues: 1-580 <WRS.
A;Taile: Differential regulation of a hydroxyproline-rich glycoprotein gene family in A;Reference number: A29356; MUID:88142825; PMID:3437892
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                                                             14;
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                                                                                                                                                                                                    HAGHDH----AddDH---AdHDH----AddDH---AdHDH----AddDH----AdHDH----Ad
                                                                                                                                                                                                                                          107 PPPYYYHSPPPPYYYHSPPPPYYYHSPPPPYYYHSPPPPYYYHSPPPPYYYHSPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 'N',1-229 <COR>
A;Cross-references: EMBL:M18094; NID:g169346; PIDN:AAA33764.1; PID:g169347
                                                                                                           6 НКРРРИСНИР-----НСРРРИСНИР-----НСРРР-----НСРРРИСР
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               432;
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C, Superfamily: hydroxyproline-rich glycoprotein
C, Keywords: glycoprotein; hydroxyproline
F):1.29, boanin: signal sequence #status predicted <SIG>F):30-580/Product: extensin #status predicted <MAT>
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33.8%; Score 235.5; DB 2;
Best Local Similarity 41.7%; Pred. No. 7.6e-11;
Matches 58; Conservative 2; Mismatches 32;
            Score 235.5; DB 2;
Pred. No. 5.9e-11;
2; Mismatches 32;
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               33.8%;
ilarity 41.7%;
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Matches 58; Conserv
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A; Accession: A05261
A; Molecule type: DNA
A; Residues: 35-39, 'P, 41-84,'G',86,'R',87-154,'R',218-246;300-306,'T',308-329,'C',331-38
A; Recession: A05262
A; Molecule type: DNA
A; Residues: "N',57-59,'A',61-69;334-336,'S',338-339,'R',341-392 <AZ5>
A; Rixuffman, D:; Mong, R.; Bennick, A.; Keller, P.
Biochemistry 21, 6556-656, 1982
A; Title: Basic proline-rich proteins from human parotid saliva: complete covalent struct A; Reference number: A00464
MUD:83101329; PMID:6924859
A; Contents: IB-9
A; Contents: IB-9
A; Accession: A90464
A; Molecule type: protein
A; Residues: 92-127,'R', 129-148,'R', 150-152 <KA3>
B; Saltoh, B.; Sanada, K.
J; Biochem: 91, 2067-2075, 1982
A; Title: Fractionation and characterization of basic proline-rich peptides of human parch A; Recence number: A91966; MUID:83007119; PMID:7118863
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A,Molecule type: protein
A,Residues: 92-127,'R',129-148,'R',150-152 <ISE>
C;Comment: This peptide contains 21-residue repeats, two of which have internal 7-residu
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NyAlternate names: hydroxyproline-rich glycoprotein
C.Species: Glycine max (soybean)
C.Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-Jul-2002
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R;Ahn, J.H.; Choi, Y.; Kwon, Y.M.; Xim, S.G.; Choi, Y.D.; Lee, J.S.
Plant Cell B, 1477-1490, 1996
A;Title: A novel extensin gene encoding a hydroxyproline-rich glycoprotein A;Reference number: Z15809; MUID:96434536; PMID:8837503
A;Accession: T06782
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Pred. No. 5.5e-11;
4; Mismatches 39;
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A;Molecule type: DNA
A;Residues: 1-432 <AHN>
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Gene: GDB:PRB1
;Cross-references: GDB:119511; OMIM:180989
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C, Keywords: glycoprotein; hydroxyproline
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Best Local Similarity 41.4%;
Matches 48; Conservative
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Query Match 33.6%; Score 234.5; DB 2; Length 173; Best Local Similarity 51.7%; Pred. No. 3.3e-11; Matches 45; Conservative 7; Mismatches 22; Indels 13; Gaps
submitted to the Protein Sequence Database, August 2000 A; Reference number: 225394
A; Accession: T51469
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-173 < SAT>
A; Cross-references: BMBL: AL391151
A; Experimental source: cultivar Columbia; BAC clone K10A8
C; Genetics:
A; Map position: 5
A; Introns: 97/1
A; Note: K10A8_130
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75 YPPAGYPAHGYPSHGYPRPSHSGHHHG 101 දි දු

67 РРРИСИРРИСРРИСИРРИСИСКИНОНС 93

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Search completed: September 23, 2004, 22:55:57 Job time : 20.2811 secs

137

us-10-074-225a-6.rsp

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 23, 2004, 21:27:50; Search time 11.7631 Seconds (without alignments) 447.085 Million cell updates/sec Run on:

US-10-074-225A-6 697 1 SVNIIHRPPPHGHHPHGPPP........HPPHGHGFHDHGPCDPPSHK 101 Title: Perfect score: Sequence:

BLOSUM62 Gapop'10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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# ALIGNMENTS

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MEDITINE=94245171; PubMed=8188234;
Hennis B.C., Frants R.R., Bakker E., Vossen R.H., van der Poort E.W.,
Blonden L.A., Cox S., Khan P.M., Spurr N.K., Kluft C.,
"Evidence for the absence of intron H of the histidine-rich
glycoprotein (HRC) gene: genetic mapping and in situ localization of
Genomics 19:195-197(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86216149; PubMed=3011081;
Koide T., Foster D.C., Yoshitake S., Davie E.W.;
Amino acid sequence of human histidine-rich glycoprotein derived
from the nucleotide sequence of its cDNA.";
Biochemistry 25:2220-2225(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                      (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
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10-MRR-1987 (Rel. 04, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Histidine-rich glycoprotein precursor (Histidine-proline rich
glycoprotein) (HPRG).
                                                                                                                                                                                                                                                                          100.0%; Score 697; DB 1; Length 526; 100.0%; Pred. No. 5.1e-41;
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Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                           810F23D367D93D42 CRC64;
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Electrophoresis 13:707-714(1992).
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 Homo sapiens (Human)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                  coagulation cascade.
SUBCELULIAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma DOMAIN: In addition to having a high His and Pro content, this protein has many internal repeats. 12 tandem repetitions of a 5-residue sequence (GHHPH, consensus) form a histidine-rich region.
SIMILARITY: Contains 2 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 КРРЕКРИGSRDHHHPHKP----НЕНФРРРРБВВВВВВРБРБРБРББРББРВ СSSCQH
FUNCTION: The physiological function is not yet known. It binds heme, dyes and divalent metal ions. It can inhibit rosette formation and is known to interact with hepatin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HWW kinlinogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000010; Cystatin.
Pfam; PF00011; cystatin; 1.
SMxRT; SM00043; CY; 2.
SJYcoprotein; Heparin-binding; Repeat; Signal; Polymorphism.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 314; DB 1; Length 525;
Pred. No. 3.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 КРР--РИС----НИРИСРРИСИИРИСРРР-----ИСИР-РИСРРР-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HISTIDINE-RICH GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P -> S (in dbSNP:3181917)
/FIId=VAR_014528.
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M13149; AAA52694.1; -.
EMBL; AB005803; BAA21613.1; -.
EMBL; Z17218; CAA78925.1; -.
PIR; A01287; KGHUGH.
SWISS-ZDPAGF; P04196; HUMAN.
Genew; HGNC:5181; HRG.
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136
2254
321
504
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241
2417
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87
125
344
345
204
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Best Local S:
Matches 64,
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396 AA

PRT;

STANDARD;

HR 303

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SEQUENCE FROM N.A
                                                                          NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                      Repeat; Parotid
SIGNAL
                                                                                                                                           TISSUE=Parotid
302
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                                                                                                                                                                                                                                                                                                                                                                                242 CPHPPFGTKGNHRPFHDHSSDEHHPHGHHPHGHHPHGHHPPGNDFYDHGPCDPPP 301
                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                    Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Histidine-rich glycoprotein (Histidine-proline rich glycoprotein)
                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                             37.3%; Score 260; DB 1; Length 396; 42.6%; Pred. No. 1.3e-11; ive 4; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                    11 HGHHPHGPPP-----HGHHPHG-----PPPHGHPPHG-----
                                                                                                                                                                                                                                                                                                                   128A8223499DE6FC CRC64;
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PRO/HIS-RICH.
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396 AA;
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                           (HPRG) (Fragments)
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Best Local Simil
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13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1087 (Rel. 05, Last sequence update)
Acidic proline-rich protein PRP33 precursor.
Rattus norvegicus (Rat).
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. Gaps MEDLINE=86033799; PubMed=3840480; Carlenents S., Mehansho H., Carlson D.M.; "Novel multigene families encoding highly repetitive peptide "Novel multigene families encoding highly repetitive peptide sequences. Sequence analyses of rat and mouse proline-rich protein POTENTIAL.
ACIDIC PROLINE-RICH PROTEIN PRP33.
6 X 18 AA APPROXIMATE TANDEM REPEATS. "Nucleotide sequence analysis of a proline-rich protein cDNA and peptide homologies of rat and human proline-rich proteins."; J. Biol. Chem. 259:10475-10480(1984). 23; PQGGPQQRPPQGFPPQG-GPQGPPQGPPQGBPPQGGHQQRPPQP 184 Score 247.5; DB 1; Length 206; Pred. No. 5.5e-11; MEDLINE=84289443; PubMed=6547951; Ziemer M.A., Swain W.F., Rutter W.J., Clements S., Ann D.K., Carlson D.M.; PHGHP-----PHGPPPHGHPPHGPPPHGHP--PHGHGFHDHGPCDP Indels cDNAs."; J. Blol. Chem. 260:13471-13477(1985). -!- FUNCTION: May protect teeth by binding to tannins. D037582CED05CE6B CRC64; 30; gland; Multigene family; Signal. 206 AA 4; Mismatches 21403 MW; 35.5%; EMBL; KO2247; AAA41949.1; -. EMBL; M11898; AAA41958.1; -. PIR; A03296; PIRT3. 53; Conservative STANDARD; TISSUE=Parotid gland; MEDLINE=84289443; Publ 206 AA; Similarity

PRP2\_MOUSE

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Gaps

41;

DB 1; Length 296; Indels

35.4%; Score 246.5; DB 1; 43.6%; Pred. No. 8.5e-11; tive 0; Mismatches 34;

Similarity 43.6 58; Conservative

Query Match Best Local

Matches

7F146824E8AF3269 CRC64;

SEQÜENCE

EMBL; M12100; AAA40005.1; -.

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MGD; MGI:97773; Prh1

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О
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 GPPPPGGPQPRPPGGPPPPGGPQRPPPPGGPQPRPPQGPPPPGGPQLRPPQGPPP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 RPPPSGFQPRPPVNGSQQGPPPPGGPQPRPPQGPPPGGPQPRPPQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 ---DHddh----Bhddbbddh----Bhdddbhddh----Bhdddbhddh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 крррнснир-----нсрррнс----ннрнсрррнс----нррнсррр-----кнррн
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                   "The structure and organization of a proline-rich protein gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.4%; Score 246.5; DB 1; Length 261; 43.6%; Pred. No. 7.7e-11; Live 0; Mismatches 34; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROLINE-RICH PROTEIN MP-2. 36E13BA7387F47D4 CRC64;
                           3-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                       mouse multigene family.";
J. Biol. Chem. 260:15863-15872(1985).
                                              10-OCT-2003 (Rel. 42, Last sequence
Proline-rich protein MP-2 precursor.
PRH1 OR PRP.
                                                                                                                                                                                                   SEQUENCE FROM N.A, MEDLINE=86059475; PubMed=2999141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 POT
261 PRC
26034 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M12099; AAA40004.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 PAGPQPRPPQGPP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 -HGFHDHGPCDPP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Conservative
                                                                                                                                                                                                                                       Ann D.K., Carlson D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:97773; Prh1.
                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 AA;
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MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Best Local
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                                                                                                                                                                                                                                         72 сырырссырдыны барырын тарарын тарасын тарас
7 RPPPHGHHP-----HGPPPHG----HHPHGPPHG-----RHPPHGPPHG-----RHPPH 45
                                                                            12 RPPPSGSQPRPPVNGSQQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPQGPQPRPPQ 71
                                                                                                                                                            98 --- DHddH---- DHdddDHddH---- DHdddDHddH---- DHdddD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 69-309 FROM N.A.
Franssen H.J., Nap J.-P., Gloudemans T., Stiekema W., van Dam H.,
Govers F., Louwerse J., van Kammen A., Bisseling T.;
Govers F., Louwerse J., van Kammen A., Bisseling T.;
Govers F., Louwerse J., van Kammen A., Bisseling T.;
Involved in early stages of root nodule development.";
Proc. Natl. Acad. Sci. U.S.A. 84:4495-4499(1987).
-!- FUNCTION: NODULIN N-75 IS INVOLVED IN EARLY STAGES OF ROOT NODULE
DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (Soybean).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Wayne;
MEDLINE=91122483; PubMed=2101308;
Franssen H.J., Thompson D.V., Idler K., Kormelink R., van Kammen A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- INDUCTION: During nodulation in legume roots after Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bisseling T.; "Nucleotide sequence of two soybean ENOD2 early nodulin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1988 (Rel. 08, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ELLY nodulin 75 precursor (N-75) (NGM-75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding Ngm-75.";
Plant Mol. Biol. 14:103-106(1990).
                                                                                                                                                                                                                                                                                                                                                                                                          132 PGGPQPRPPQGPP 144
                                                                                                                                                                                                                                                                                                                             87 -HGFHDHGPCDPP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3847;
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"The structure and organization of a proline-rich protein gene of

mouse multigene family."; J. Biol. Chem. 260:15863-15872(1985).

SEQUENCE FROM N.A.
MEDLINE=86059475; PubMed=2999141;
Ann D.K., Carlson D.M.;

NCBI TaxID=10090;

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

, Last sequence update) , Last annotation update)

13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last seq. 10-OCT-2003 (Rel. 42, Last anno

Proline-rich protein MP-3 (Fragment). PRH1 OR PRP.

(Wouse)

musculus

296 AA

STANDARD;

PMP3 MOUSE P05143;

PMP3\_MOUSE

RESULT

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7;
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                                                                                                                                                                                                                                                                                               КРРРЕУОРРИВКРРИ---- ЕМРРРЕНОРРИЕКРРЕНОРРИЕКРРЕУЕРРЕУЕРРЕУОР 150
                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                 MEDILINE=8161834; PubMed=6671974;
Saitoh E., Isemura S., Sanada K.;
"Further fractionation of basic proline-rich peptides from human
parotid saliva and complete amino acid sequence of basic proline-rich
J. Biochem. 94:1991-1997(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maeda N., Kim H.-S., Azen E.A., Smithies O.;
Differential RNA splicing and post-translational cleavages in the
human salivary proline-rich protein gene system.";
J. Biol. Chem. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-1987 (Rel. 04, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary proline-rich protein precursor (Clones CP3, CP4 and CP5)
[Contains: Basic peptide IB-6; Peptide P-H].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kauffman D., Hofmann T., Bennick A., Keller P.;
"Basic proline-rich proteins from human parotid saliva: complete
covalent structures of proteins IB-1 and IB-6.";
Biochemistry 25:2387-2392(1986).
                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                   Length 309;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                             64 РН-GРРРНGНРРН-GРРРНGНРРНGНGFC--DPPSHK 101
                                                                                                                                                                                                                                                                                                                                                            151 РИВКРРРЕУОРРИНКРРРЕУОРРИВКРРРЕНОРРИНКРРЕНО 192
                                                                                                                                      EARLY NODULIN 75,
Y -> C (IN REF. 2).
2773D28CCBDE1654 CRC64;
                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                     Score 233.5; DB 1
Pred. No. 6.6e-10;
                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          331 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=85289325; PubMed=2993301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 214-331.
MEDLINE=86243355; PubMed=3521730;
                                            35966 MW;
                                                                                                                                                                                                   33.5%;
48.0%;
             EMBL; M16976; AAA33996.1; -.
EMBL; X16875; CAA34758.1; -.
EMBL; X16876; CAA34759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K03204; AAA60185.1; -. EMBL; K03205; AAA60186.1; -.
                                                                                                                                                                                                                  Local Similarity 48.0
les 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                      309 AA;
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                                                                                                                                                                       SEQUENCE
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MEDILINE=22388257; PubMed=12477932;

Atlasoure R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Atlaschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Mark J. M., Gay L.J., Hulyk S.W.,
Kichards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
Kichards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
A Whiting M., Madan A., Sodergren E.J., Lu X., Gibbs R.A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Generation and initial analysis of more than 15,000 full-length
Human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                      101 PPQGGNQPQGPPPPGKPQGPPPQGGNKPQGPPPPGKPQGPPPQGDKSQSPRSPPGKPQG 160
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                                                                                                                                                                                                                                                                                                                                                   8 РЕРНСИНРИСРЕРИСИНРИСРЕРИ-СИРРИСРЕРКИРРИСРЕРИСИ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Splicing factor 3B subunit 4 (Spliceosome associated protein 49)
49) (SF3b50) (Pre-mRNA splicing factor SF3b 49 kDa subunit).
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MEDIJINE-95047348; PubMed=7958871;
Champion-Arnaud P., Reed R.;
"The presplicesome components SAP 49 and SAP 145 interact in a complex implicated in tethering U2 snRNP to the branch site.";
                                                                                                                                                                                                                                                                          Score 233.5; DB 1; Length 331;
Pred. No. 7e-10;
4; Mismatches 38; Indels 25;
                                                                                                     PEPTIDE IB-6.
PEPTIDE P-H.
Missing (in clone CP-4).
/FTIG+VAR 005561.
Missing (In clone CP-5).
/FTIG+VAR 005561.
A > S (IN REF. 2 AND 3).
W, 3F481FF8EBA39751 CRC64;
                                                                    gland; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 AA
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4; Mismatches
                                                                                                                                                                                                                                       331 AA; 32596 MW;
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Genes Dev. 8:1974-1983(1994).
                                                                                                                                                                                                                                                                          33.5%;
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                                 Genew; HGNC:9337; PRB1.
                 PIR; B40750; PIHUB6.
                                                                                                                                                                                                                                                                                            Local Similarity
tes 49; Conserv
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                                                  Repeat; Parotid g
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                                                                                                                           276
106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S3B4 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                       SEQUENCE
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SEQUENCE FROM N.A.
401 LPPP 404
                                                                                                                                      NCBI_TaxID=9606;
                                         PRP2_HUMAN
P02812;
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SEQUENCE
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                                   PRP2_HUMAN
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                                                345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 PGHGHSHPHPPPPGGMPHPGMSQMQLAHHGPHGLGHPHAGPPGSGGQPPPRPPGMPHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   YEAST HSH49.
SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; 1.
Spliceosome; mRNA processing; mRNA splicing; Nuclear protein;
                  MEDLINE=20337962; PubMed=10882114;
Das R., Zhou Z., Reed R.;
"Functional association of UZ ShRNP with the ATP-independent spliteosomal complex E.";
Mol. Cell 5:779-787(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Indels
                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005681; C:spliceosome complex; TAS.
GO; GO:0008248; F:pre-mRNA splicing factor activity; TAS.
GO; GO:0006371; P:mRNA processing; TAS.
GO; GO:0006371; P:mRNA splicing; TAS.
InterPro; IPR000564; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
SMART; SM00360; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212472A25D3FF002 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA-BINDING (RRM) 1
RNA-BINDING (RRM) 2
POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 233.5; DB 1
Pred. No. 8.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
  (3)
CHARACTERIZATION OF THE SPLICEOSOME.
                                                                                                                                                                                                                                                                                               EMBL; L35013; AAA60300.1; -.
EMBL; BC004273; AAH04273.1; -.
EMBL; BC013886; AAH13886.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44385 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.5%;
46.0%;
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179
218
268
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215 2
262 2
424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-binding; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 CDPP 98
                                                                                                                                                                                                                                                                                                                                                   GK; Q15427; -.
MIM; 605593; -
                                                                                                                                                                                                                                                                                                                                   HSSP; P11940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                               21-UUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2001 (Rel. 41, Last annotation update)
peptide P-F] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83265674; PubMed=6874669; Saitoh E., Isemura S., Sanada K.; Scitoh E., Isemura S., Sanada K.; "Complete amino acid sequence of a basic proline-rich peptide, P-F, from human parotid saliva."; J. Biochem. 93:883-888 (1983).
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-85289325; PubMed-2993301;
Maeda N., Kim H.-S., Azen E.A., Smithies O.;
Differential RNA splicing and post-translational cleavages in the
human salivary proline-rich protein gene system.";
J. Biol. Chem. 560:11123-11130(1985).
                                                                                                                                                                                                                                            Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 GPPPH-GHPPHGPPHGHPPHGHPHGH-----РРИGНGFHDHGPCDPP 98
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Pred. No. 1e-09;
3; Mismatches 34; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24641 MW; D779F590C0EBF30B CRC64;
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21-UUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AA
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NON TER 1 1 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; K03208; AAA60189.1; -.
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STANDARD;
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Genew; HGNC:9338; PRB2.
                                                                                                                                                                                                                          Homo sapiens (Human)
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251 AA;
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PRB4_HUMAN
ID PRB4_HT
AC P1016-3
DT 21-JUL-1
DT 28-FEB-
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01-MAR-1989
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P10161; P02
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                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPPQGGNQSQGPPPHPGKPERPPPQGGNQSQGTPPPPGKPERPPQGGNQSHRPPPPPGK 140
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                                                                                                                                                                                                                                                                                                           MEDLINE=89121440; PubMed=2851479;
Lyons K.M., Stein J.H., Smithies O.;
"Length polymorphisms in human proline-rich protein genes generated
by intragenic unequal crossing over.";
Genetics 120:267-278(1988).
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10.10162, P0.02813,
01.MAR-1999 (Rel. 10, Last sequence update)
01.MAR-1999 (Rel. 41, Last annotation update)
Salivary proline-rich protein PO (Allele K) [Contains: Peptide P-D] (Fragment).
                                                                                                                                                                                                           the
                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                               MEDLINE-85289325; PubMed=2993301;
Maeda N., Kim H.-S., Azen B.A., Smithies O.;
"Differential RNA splicing and post-translational cleavages in
human salivary proline-rich protein gene system.";
J. Biol. Chem. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Parotid gland; Multigene family; Glycoprotein; Signal.
SIGNAL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SALIVARY PROLINE-RICH PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Indels
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MISSING (IN REF. 2).
D -> A (IN REF. 2).
; 6A1943E43E161691 CRC64;
    (S)
Salivary proline-rich protein PO precursor (Allele PRB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 228; DB 1;
Pred. No. 1.3e-09;
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ilarity 36.4%;
Conservative
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MIM; 168730; -.
MIM; 180990; -.
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247
39
177
57
                                           Homo sapiens (Human)
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                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=9606;
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CONFLICT
SEQUENCE
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Best Local S:
Matches 52
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ID PRPL HI
AC 01.042,
DT 01.042,
DT 01.048,
DE Salivan
DE (Fragmi
GN PRB4.
GN PRB4.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENDL Outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 RPPOGGNOSOGPPPHPGKPERPPPOGGNOSHRPPPPGKPERPPPGGGNOSOGPPPHPGK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 ÞEGÞPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQAPPA 250
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Lyons K.M., Stein J.H., Smithies O.;
"Many protein products from a few loci: assignment of human salivary
proline-rich proteins to specific loci.";
Genetics 120:255-265(1988).
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28-FBB-2003 (Rel. 41, Last annotation update)
Salivary proline-rich protein PO (Allele M) [Contains: Peptide P-D]
                                                                                                                                                                                                                                                                                                  SEQUENCE OF 207-276.
WEDLINE-S18612.P. PubMed-6841349;
Saltoh E., Issmura S., Sanada K.;
"Complete amino acid sequence of a basic proline-rich peptide, P-D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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Eutheria, Primates; Catarrhini; Hominidae; Homo.
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276 AA; 27816 MW; 9F494926C97941A CRC64;
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Lyons K.M., Stein J.H., Smithies O.;
"Many protein products from a few loci: assignment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PR00929, ATHOOK.
Repeat, Parotid gland, Multigene family.
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InterPro; IPR000637; AT_hook.
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PIR; S03176; PIHUSD.
MIM; 168730; -.
MIM; 180990; -.
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(Rel. 34, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biochem. 93:495-502(1983)
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es 50; Conserv
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                                                                                      SECUENCE FROM N.A.
                               NCBI_TaxID=9606;
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EMBL; X55371; CAA39050.1; -
PIR; S11967; S11967.
Nodulation; Repeat.
NON TER
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P13983;
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                                                                                                                                    Query Match
Best Local
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                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 RPPPPGKRPGGPPPQGGNQSQGPPPHPGKPERPPQGGNQSQGPPPHPGKPERPPPQGGN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lupinus luteus (Yellow lupine).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids 1; Fabales, Fabaceae, Papilionoideae, Genisteae, Lupinus.
NCBI_TaxID=3873;
                                                                    MEDLINE=83186122; PubMed=6841349;
Saltoh E., Isemura S., Sanada K.;
"Complete amino acid sequence of a basic proline-rich peptide, P-D,
from human parotid saliva.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUB=Root nodules;
TISSUB=Root nodules;
SECRYGIOWEKI K., Legocki A.B.;
"Isolation and nucleotide sequence of cDNA clone encoding nodule-specific (hydroxy) proline-rich protein LENOD2 from yellow lupin.";
Plant Mol. Biol. 18:361-363 (1990).
-!- FUNCTION: INVOLVED IN EARLY STAGES OF ROOT NODULE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 РРИСРРИСИРРИСРРИ-СИРРИСРРИ----СИРРИСРИРИ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 221.5; DB 1; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 OSOGPPTPGKPEGPPPQGGNQSQGPPPHPGKPERPPPQGGNQSHRPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last annotation update)
Early nodulin 75 protein (N-75) (NGM-75) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                    434 AA
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
      proline-rich proteins to specific loci."; Genetics 120:255-265(1988).
                                                                                                                                                                                                                                                                                                                      MIM; 180990; -. Goxtracellular; NAS. GO; GO:0005576; C:extracellular; NAS. Repeat; Parotid gland; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                            23676 MW;
                                                                                                                                    93:495-502(1983)
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Duest Local Similarity 42.50,
Best Local 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                234
                                                     SEQUENCE OF 165-234.
                                                                                                                                                                                                                                                                                                                                                                                                               234 AA;
                                                                                                                                     J. Biochem.
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NO75 LUPLU
Q06841;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        137 LVH-РРРНОКРРІБҮНРРНЕКРРІВУРРНЕКРРІВУРРІВУРРНЕКРРІВУРРИЖЕР 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 РҮЗКРРРУНРРРОЗКРРІЗУРРРІЗКРРУНЕРРУЗКРРРАОРРЯОКРІЗУРРНЕКРР 255
                                                                                                                                                                                                                                                                          43
                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Extracellular matrix.
THE EXTRENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-REO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana tabacum (Common tobacco).
Bukaryote, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                          4 IIHRPPPHG-----HHPHG-----PPPHGHHP-HGPPPHGHPPHGPPRH-----P
                                                                                                                                                                                                                                                                                                                                                                                                             ------
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Extensin precursor (Cell wall hydroxyproline-rich glycoprotein).
                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycoprotein gene in lateral root initiation.";
Genee Dev. 3:1639-1646[1989].
-!- FUNCTION: Has a specialized structural function, possibly the mechanical penetration of the cortex and epidermis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRSUB=Leaf; STRAIN=cv. Xanthi; TISSUB=Leaf; STRAIN=cv. Xanthi; PubMed=2612909; Keller B., Lamb C., T., Keller B., Lamb C., T., Specific expression of a novel cell wall hydroxyproline-rich
36 X 8 AA APPROXIMATE REPEATS OF
                                                                                                                                      434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat, Cell wall; Glycoprotein; Signal; Structural protein; Hydroxylation.
                                                                                                                                                                                                        40; Indels
                                                                                                                                      DB 1; Length
                                P-P-H-E-K-P-P.
8CE8E140C21B6664 CRC64;
                                                                                                                               Score 210.5; DB 1
Pred. No. 3.1e-08;
6; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
EXTENSIN.
H-A-P-P.
H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 -HGHGFHDHGPCDPPSHK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 VYEPPYERSPPVHPPSHE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000480; Glutelin.
PRINTS; PR00211; GLUTELIN.
                                                              434 AA; 49827 MW;
                                                                                                                                   30.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 44 PHGPPPHGHPP-----
                                                                                                                                                                                                        51; Conservative
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620
73
151
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
70
148
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REPEAT
REPEAT
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Query Match
Best Local Similarity 42.3%; Pred. No. 4.4e-08;
Matches 55; Conservative 4; Mismatches 29; Indels 42; Gaps 13;
                                                                                             2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
Search completed: September 23, 2004, 22:50:36 Job time : 12.7631 secs
                                                                                                                                                  91 DHGPCDPPSH 100
                                                                                                                                                            177 -HPP--PPTY 183
DOMAIN
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September 23, 2004, 22:25:45; Search time 59.6265 Seconds (without alignments) 534.449 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
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US-10-074-225A-6 697 1 SVNIIHRPPPHGHHPHGPPP.......HPPHGHGFHDHGPCDPPSHK 101 Scoring table: Title: Perfect score: Sequence:

1017041 segs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries SPTREMBL Database :

p\_maximual: sp\_mth:\* sp\_organelle:\* sp\_organelle:\* sp\_plant:\* sp\_virus:\* sp\_virus:\* sp\_vortebrate:\* sp\_vortebrate:\* sp\_vortebrate:\* sp\_vortebrate:\* sp\_vortebrate:\* sp\_roteriap:\* sp\_roteriap:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fung!:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Q9bgul bos taurus	Q99ps8 rattus norv	O39pse mus musculu		Q99ps5 mus musculu	Q99ps7 rattus norv	Q9esb2 rattus norv	Q07611 rattus norv	Q95jd0 sus scrofa	Q95jdl sus scrofa		Q62107 mus musculu	Q62103 mus musculu	Q04154 rattus norv	Q9cr74 mus musculu	Q41402 sesbania ro
ΩI	Q9BGU1	099PS8	984660	Q9ESB3	Q99PS5	Q99PS7	Q9ESB2	007611	Q95JD0	Q95JD1	695409	062107	062103	Q04154	Q9CR74	041402
DB	9	11	11	11	11	11	11	11	9	9	9	11	11	11	Η	10
° Query Match Length DB	546	525	525	525	525	515	510	295	511	566	676	227	317	274	112	330
Query Match	60.3	53.8	47.8	47.8	47.8	46.3	45.2	37.2	37.1	37.1	36.5	35.4	35.4	35,3	34.7	33.9
Score	420.5	375	333	333	333	323	315	259.5	258.5	258.5	254.5	246.5	246.5	246	242	236
Result No.		0	m	4	IJ	φ	7	œ	0	10	11	12	13	14	15	16

homo sapi	Q39835 glycine max		arab	ОШО	ошо	Osazyo mus musculu	mus	Q8r5n0 mus musculu	mus,	Q15214 homo sapien	homo	·O	9	Q9vpz1 drosophila	O00600 homo sapien	Q9vep4 drosophila	Q9fur6 cladrastis	homod				Q91x93 mus musculu	ictyostel	Q9lj64 arabidopsis	Q8mp30 dictyosteli	ᄃ	122	Q9fi79 arabidopsis
208805	039835	000083	Q9LF59	016038	OBEYAL	080ZY9	054978	OBRSNO	Q80U47	015214	000599	Q9VUE1	062106	Q9VPZ1	009000	Q9VEP4	Q9FUR6	004118	Q61138	Q9FUR7	062105	Q91X93	Q861N4	Q9LJ64	Q8MP30	059907	041122	Q9FI79
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358	432	580	173	297	338	424	1571	1572	1617	173	382	102	188	80	238	594	244	3.09	1378	269	301	504	1749	926	233	472	297	205
33.8	33.8	33.8	33.6	33.5		33.5	33.4	33.4	33.4	33.1	33.1	32.8	32.8	32.3	32.1	32.0	31.9	31.7	31.7	31.3	30.6	30.5	30.5	30.3	30.3	30.3	30.1	30.1
235.5	235.5	235.5	234.5	233.5	233.5	233.5	232.5	232.5	232.5	231	230.5	228.5		22	224	223	222.5	22	221	218.5	-:	212.5	212.5	211.5	211	211	210	209.5
17	18	13	20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	32	36	3.7	80	9.0	40	41	42	43	44	45

# ALIGNMENTS

																						2;	26	396		
	PRELIMINARY; PRT; 546 AA.	(TrEMBLrel. 17, Created) (TrEMBLrel. 17, Last sequence update)	Last	Histidine-rich glycoprotein. Dans	(Bovine)	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	utheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	vinae; Bos.	.9913;		kahashi K., F	Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;	"Molecular diversity of mammalian histidine-rich glycoprotein.";	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.		GO; GO: 0004869; F: cysteine protease inhibitor activity; 1EA.	Interpro; IPR00010; Cystatin.	Pfam; PF00031; Cystatin; 1.			60.3%;	nijarity 53.8%; rred. NO. 1.18-32; Conservative 4; Mismatches 21; Indels 13; Gaps	НКРРРИСИНРИСРРРИСИНРИСРРИСИРРИСРРИСРРИСРРИСР	нкрририssdенирнанирнанирнанирнанирнандрнанирнанирнания 396	PPPHGHPPHGHPPHGPPHGHPPHGHGFHDHGPCDPSHK 101	397 HHPHGHHPHGHHPHGHHPHGHHPHDNDFYDHGPCDPPPHR 441
1 11	Q9BGU1	01-JUN-2001	01-JUN-2003	Histidine-r	Bos taurus	Eukaryota; Metazoa;	Mammalia; Eutheria;	Bovidae; Bovinae;	NCBI_TaxID=9913;	SEOUENCE FROM N.A.	Wakabayashi	Ohashi T.,	"Molecular	Submitted	EMBL; AB055	90; 90:000	InterPro;	Pram, Proof	SMAKI; SMCCO45; CI;	SECUENCE		Best Local Sir Matches 67;	H 9	341 H	57 PI	397 田
RESULT	O A	IQ E	Ιď	E S	SO	8	Ö	ဗ	X N	R	B	RA	RT	됬	DR	DR	Ä	Z :	¥ (	Š	8	X Be	ò	Db	ò	Q

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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Conservative
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW413091 OR HRG.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                       Q9ESB3
Q9ESB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Q99PS5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                   RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 NRSHR-РРНИНЅСИЕНРСНСОНРИСНИЕНРНОННРНСОНРНСНИРНСОНРНСОНРНСОНРНСТИРНС 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NI I Н К РРРИСН - - - НР - Н СРРИСНИРИСРРИСИРОНСРРИС - - - НР РИСРРИС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.8%; Score 333; DB 11; Length 525;
ilarity 58.3%; Pred. No. 2.46-24;
Conservative 3; Mismatches 30; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague. Dawley; TISSUE-Liver; Makabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S., Ohashi T., Sato N., Hirate D., Tsuchida N., Kodide T.; Ohashi T., Sato N., Hirate D., Tsuchida N., Kodide T.; Molecular diversity of mammalian histidine-rich glycoprotein."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB055895; BAB31092.11, -
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA. InterPro: IPR00010; Cystatin.
InterPro: Cystatin; 1.
SNART; SM00043; CY; 2.
SEQUENCE 525 AA; 59049 MW; 38290A631FAC7777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DECEMBER FROM WASTER TISSUE-Liver;
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S., Makabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S., Mashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S., Mashi J., Sato N., Hirate D., Tsuchida M., Koidg T., Malecular diversity of mammalian histidine-rich der T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
MGD; MGD: SBSS 5897; BAB33094.1; -.
MGD; MGI: 2146636; PROSTERING PROSTERING ACTIVITY; IEA.
GO; GO: 0004869; F: Cysteine protease inhibitor activity; IEA.
Fram: PF00031; Cystein.
Fram: PF00031; Cystein.
SMART; SM000445; YY; S.
SEQUENCE 525 AA; 59090 MW; AB3E93A439CFB3AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 РРРИСИРРИСРРИСИРРИСРРИСИРРИСИРРИСИВИСИВРЅИ 100
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01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UTN-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein.
AW413091 OR MMHRG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.8%; Score 375; DB 11;
63.5%; Pred. No. 2.4e-28;
live 2; Mismatches 24;
                                                                              525 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.5
Matches 66, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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                                                                       099PS8
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RESULT 2
299PS8
10 099PAC
299PBAC
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201-J
DT 01-J
DT 01-
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hulett M.D., Parish C.R.; "Murine histidine-rich glycoprotein: cloning, characterization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.8%; Score 333; DB 11; Length 525; 58.3%; Pred. No. 2.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TSuchlida N., Wakabayashi S., Jahnen-Dechent W., Koide T.; Tsuchida N., Wakabayashi S., Jahnen-Dechent W., Koide T.; Structure of mouse histidine-rich glycoprotein gene."; Submitted (FBB-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                           58 РРИСИРРИСРРИСИРРИСРРИСРРИСИРРИСРЕНИИСРОРРЯН 100
                                                                                                                                           377 HPPGHHPHGHHPHGHHPHGHHPHGHDFLDYGPCDPPSN 419
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                                                                                                                                                                                                                                                                                                                                                    01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Histidine-rich glycoprotein.
AW413091 OR MMHRG.
                                                    322 NRTHR-PSYNHSCNEHPCHGHRPHGHHPHSHHPPGHHSHG-
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                                                                                                                                                                                                                                                                                                     525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cellular origin.";
Immunol. Cell Biol. 78:280-287(2000)
                                                                                                                                                                                                                                                                                                     PRT;
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18; Gaps

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81 VNRPERPPQHGGNHHHPHHPPPPAAGPQRPPQPGSPQGPPPGGPQQRPPQGPPQGGPQR 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 NRSHRPPRNHSCNEHPCHRQHPHGHHPHGQHPHGHHPHGQHPR------GHHPHGQH 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NIIHRPPPH---GHHP-нGPPPHGHHPHGPPPHGHPPHGPPRHPPHGPPPHGPP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEAIN-Sprague-Dawley, TISSUE-Parctid gland;
MEDLINE=93388626; PubMed=8376404;
Castle A.M., Castle J.D.;
"Novel secretory polline-rich proteoglycans from rat parctid. Cloning and characterization by expression in AtT-20 cells.";
J. Biol. Chem. 268:20490-20496(1993).
EMBL; LI7318; AAA03074.1; --
PIR; B48013; B48013.
SEQUENCE 295 AA; 30026 WW; EEA44BD8B38E1B9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 -----РИСРР-----РИСРРИСРРИСНР-----РИСРРРИС
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                     STRAIN=Lewis;
STRAIN=Lewis;
MEDLINE=20307726; PubMed=10849117;
Hulett M.D., Parrish C.R.;
Hulett M.D., Parrish C.R.;
Hular origin.";
Final article histidine-rich glycoprotein: cloning, characterization and cellular origin.";
Final AF14029; AAG38417.1;
Final AF144029; AAG38417.1;
Final AF14029; Progretine protease inhibitor activity; IEA.
InterPro; IPR000010; Cystatin.
SMART; SM00031; Cystatin; 1.
SMART; SM00033; CY; 2:
SEQUENCE 510 AA; 57581 MW; 508E6E06AA2ED58E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.4%; Pred. No. 1.5e-17;
Matches 63; Conservative 1; Mismatches 27; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                        45.2%; Score 315; DB 11; Length 510; 55.9%; Pred. No. 1.2e-22; tive 3; Mismatches 24; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 GPQRPPQPGSPQGPPPGGPQQRPPQGPPPQG-----GPQRPP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 HP------PHGP------98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 PRGH-----HPHGHHPHGHPHGHHPHGHDFLDYGPCDPPSN 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 РИСИРРИСРРИСИРРИСРРИСРРИСИРРИСИСЕН ПОО 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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(TrEMBLrel. 01, I
(TrEMBLrel. 25, I
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.99
Matches 57; Conservative
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                                                                                      SEQUENCE FROM N.A.
                                              NCBI TaxID=10116;
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01-NOV-1996 (
01-OCT-2003 (
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Q07611
ID Q07611
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                                                                                                                                                                                                                                                                                                                                  322 NRTHR-PSYNHSCNEHPCHGHRPHGHHPPSHSHSHG----HHPHGHHPHSHSHGH 376
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                                                                                                                                                                                                                                                                                                   3 NIIHRPPPHGH----- нР- нGPPPHGHPPHGPPPHGPPPHGPPHGPPHGP
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                           Gaps
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Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.,
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.,
Mashayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.,
Molecular diversity of mammalian histidine-rich glycoprotein.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABD55896; BAB33093.11;
EMBL; ABD55896; BAB33093.11;
InterPro; IPR00010; Cystain.
InterPro; IPR00031; Cystain.
SMART; SM00043; CY; 2.
SEQUENCE 515 AA; 58055 MW; 7CEBA3AIA3678966 CRC64;
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                                                                                                                                                                                                                    525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 NRSHR-PPHNHSCNEHPCHGQHPHGHHPHGQHPHGHHPHG---QH---
                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 HPHGHHLHRHPHGHPHGDHPHGHHPHGHDFLDYGPCDPPSN 409
                                                                                                                                                                                                                                                                                                                                                                                                           377 HPPGHHPHGHHPHGHHPHGHHPHGHDFLDYGPCDPPSN 419
                                                                                                                                                                                                                                                                                                                                                                                   58 РРНGНРРНGРРРНGНРРНGРРРНGНРРНGНGFHDHGPCDPPSH 100
    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB055898; BAB33095.1; -.
EMBL; AB01168; AAH111681; -.
MGD; MGI:2146636; AW413091.
GO; GO:0004869; F:cysteine protease inhibitor activity; InterPro; IPR00010; Cystatin.
FPEGM; PFE0031; Cystatin; 1.
SWART; SMO0643; CY; 2.
SRQUENCE 525 AA; 59162 NW; A83E93A439CFB126 CRC64;
                                                                                                                                                                                                                 Length
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                 Score 333; DB 11;
Pred. No. 2.4e-24;
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01-MAR-2001 (TrEMBLrel. 16, L6
01-JUN-2003 (TrEMBLrel. 24, L6
Histidine-rich glycoprotein.
HRG.
Rattus norvegicus (Rat).
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01-UNA-2001 (TrEMBLrel. 17, Cx
01-UUN-2001 (TrEMBLrel. 17, La
01-UUN-2003 (TrEMBLrel. 24, Le
Histidine-rich glycoprotein 2.
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Best Local Similarity 58.3%;
Matches 60; Conservative
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09ESB2
1D 09ESB1
AC 09ESB2
DT 01-M
DT 01-M
DF HIGT.
GN HRGT.
OS RALTI
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                                                                                                                                                                                                                       TISSUE=Parotid gland;
Zhang Q., Szalay A.A., Kyeyune-Nyombi E., Sands J.F., Oberg K.C.,
Tieche J.-M., Leonora J.;
"Cloning and expression of a novel proline-rich protein from porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TISSUB-Parotid gland,
Zasuby A.A., Kyeyune-Nyombi E., Sands J.F., Oberg K.C.,
Tieche J.-M., Leonora J.,
"Cloning and expression of a novel proline-rich protein from porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Basic proline-rich protein.
Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Basic proline-rich protein.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 3.4e-17;
0; Mismatches 27; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 511;
                                                                                                                                                                                                                                                                                      parotid glands. i. b. b. b. b. b. b. b. b. b. databases. Submitted (MAY-201) to the EMBL/GenBank/DDBJ databases. EMBL; AXO35848; AAK61382.1; GO: 0005199; F:structural constituent of cell wall; IEA. InterPro.; PRR0128; Pistli extensin. PRR1NTS; PRR1218; PSTLEXENSIN. SEQUENCE 511 AA; 48483 MM; AB04597964C448D7 CRC64;
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es 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parotid glands.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY038847; AAK61881.1;
GO; GO:0005199; F:structural constituent of cell wall; IEA.
INTERPRO; IPRO03882; Fistil extensin.
ENERGY: PRO1218 PSTIATENSIN.
SEQUENCE 566 AA; 53213 MW; E33B3B5E1BDEB81A CRC64;
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Last sequence update)
Last annotation update)
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                                   511 AA
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55.3%; Pred. No. 3.1e
tive 0; Mismatches
                                 PRT;
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1 Similarity 55.3%;
52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.3'
Matches 52; Conservative
                                 PRELIMINARY;
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                           NCBI TaxID=9823;
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RESULT 9
Q95JD0
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314 РРРРСРРЕФРАРДАКРРЕФРЕРБРЕРБРЕРБРЕРБТАКРРЕФЕРБЕСРБРЕСТ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Paroctid gland;

Zhang O., Szalay A.A., Kyeyune-Nyombi E., Sands J.F., Oberg K.C.,

Tieche J.-M., Leonora J.;

"Cloning and expression of a novel proline-rich protein from porcine
parotid glands.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AN015849; AAK61383.1;

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0005249; F:voltage-gated potassium channel activity; IEA.

GO, GO:0006813; P:pocassium ion transport; IEA.

InterPro; IPR005404; KV33 ChANNĒL.
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MEDLINES 66031799; PubMed=3840480;
Clements S., Mehansho H., Carlson D.M.;
"Novel multigene families encoding highly repetitive peptide sequences: Sequence analyses of rat and mouse proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 PPGPPPPGPPPGPAPPGARPPPGPPPGPPPGAPPGARPPP 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.5%; Score 254.5; DB 6; Length 6 50.9%; Pred. No. 9.5e-17; ive 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 AA; 62297 MW; 3008BC41EFD81FC9 CRC64;
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                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Basic proline-rich protein.
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Last annotation update)
                                                        343 PPGPPPGPPPGPAPPGARPPGPPPGPPPG
86
54 РИСРРИСИРРИСР-РРИСИРРИСРРИСИРРИС
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Les 54; Conservative
                                                                                                                                                                                                                  PRELIMINARY;
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Best Local Similarity
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STRAIN-C57BL/61; TISSUB-Pancreas, and Small intestine;

MIDINE-21085660; PubMed=1127851;

MIDINE-21085660; PubMed=1127851;

RAMARAWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAMARAWA T., Tawa M., Nishia Y., Komo H., Adachi J., Fukuda S.,

Alzawa K., Tawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RAMARAWA T., Salto R.,

RAMARAWA T., Matsuda H.A., Ashburner M., Bandavs T., Casavant T.,

RAMARA SARAI K., Matsuda H.A., Ashburner M., Bandavs B., Kochiwa H.,

RAMARA K., Okido T., Furuno M., Aono H., Baldavelli R., Barsh G.,

RAMARA K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RAMARA K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RAMARA SAKAI K., Dijunga N., Carninci P., de Bonaldo M.F.,

RAMARA Bake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RAMARA B., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RAMARA B., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RAMARA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

RAMARA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Warshi, Sato K., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,

Warshi, Sato K.,

Warshi, Sato K.,

Wangal M., Rawa M., Rawa M., Kawaji H., Rohtsuki S.,

Warshi, Sato K.,
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                                                      STRAIN-Sprague Dawley, TISSUE-Liver;
MEDLINE-21257817; PubMed=2045095;
Lin H.H., Ann D.K.;
"Molecular characterization of rat multigene family encoding proline-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata, Vertebrata; Euteleostomi,
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                      Length 274;
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                                                                                                                                                                                                                274 AA; 27380 MW; 6A57121F8F07387B CRC64;
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Last annotation update)
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Mammalia; Eutheria; Rodentia;
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(TrEMBLrel. 17, I
(TrEMBLrel. 24, I
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                                                                                                                                    rich proteins.";
Genomics 10:102-113(1991).
EMBL; M64793; AAA42064.1; -.
PIR; B39066; B39066.
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les 57; Conservative
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1810007E14RIK OR AA238765.
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NCBI_TaxID=10116;
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01-JUN-2003
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                                                                                                                        46 GPPPHG----НРРНGPPPHG----НРРНGPPPHG----НРРНG----НРРНG----
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN—0-1; TISSUB=Liver;
MEDLINE=88273214; Pubmed=2835509;
Ann D.K., Smith M.K., Carlson D.M.;
Molecular evolution of the mouse proline-rich protein multigene "Mollecular evolution of the mouse proline-rich protein multigene family. Insertion of a long interspersed repeated DNA element.";
J. Biol. Chem. 263:10887-10893(1988).
P. Biol. Chem. 263:10887-10893(1988).
PIRI, A28996; A28996.
MGD; MGI:1932491; Prp2.
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        34; Indels
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PROLINE-RICH PROTEIN.
019301BE31D73278 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.4%; Score 246.5; DB 11;
43.6%; Pred. No. 2.8e-16;
tive 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                            317 AA
        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Proline-rich protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salivary proline-rich protein.
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                                                                                                                                                                                                                                              153 PAGPOPRPPOGPP 165
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Best Local Similarity 43...
Best Local Similarity 63...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 -HGFHDHGPCDPP 98
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          Conservative
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                        87 -HGFHDHGPCDPP
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16 3
317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q04154;
01-NOV-1996 (
01-NOV-1996 (
01-OCT-2003 (
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          58;
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RESULT 14 Q04154

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Best Local Similarity 50.5%; Pred. No. 3e-16;
Matches 54; Conservative 0; Mismatches 39; Indels 14; Gaps
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Search completed: September 23, 2004, 22:55:05 Job time : 61.6265 secs

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September 23, 2004, 22:47:25; Search time 18.253 Seconds (without alignments) 285.664 Million cell updates/sec
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                                                                                                                                                                                                                                               US-10-074-225A-6
697
1 SVNIIHRPPPHGHHPHGPPP........
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                  389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                               Run on:
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Description	Sequence 64, Appl		235		4,	9	Sequence 4, Appli	7	Sequence 13, Appl	m	'n	'n	'n	49,	4	53	4,	Sequence 4, Appli	Τ,	ω	ή,	8	45	45	51		52
ID	US-09-976-594-64		US-09-547-693-235	US-09-281-766-19	US-08-925-237-4	US-08-217-327-6	US-08-217-327-4	US-07-945-283-2	US-09-507-323B-13	US-08-487-359-3	US-08-222-798A-3	US-08-487-359-5	US-08-222-798A-5	US-08-642-255-49	US-09-219-849-4	US-08-642-255-53	US-08-487-359-4	US-08-222-798A-4	US-08-487-359-1	US-08-487-359-8	US-08-222-798A-1	US-08-222-798A-8	US-09-461-325-453	US-10-012-542-453	US-08-642-255-51	US-09-219-849-3	US-08-642-255-52
Length DB	525 4	124 2	104 4	865 4	82 2	306 1	214 1	1958 1	167 3	79 1	79 1	78 1	78 1	144 1	720 3	777 1	79 1	79 1	79 1	79 1	79 1		148 4	148 4	234 1	504 3	561 1
% Query Match L	45.1	32.9	30.9					24.0	23.5	23.1	23.1	23.0	23.0	23.0	23.0	23.0	23.0	23.0	22.8	22.8	22.8	22.8	22.7	22.7	22.7	22.7	22.7
Score	314	229.5	215.5	208	196	175	171	167	164	161	161	160.5	160.5	160.5	160.5	160.5	160	160	159	159	159	159	158.5	158.5	158.5	158.5	158.5
Result No.	-	201	m	4	ഗ	9	7	80	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27

Seguence 2, Appli	Sequence 6, Appli	Sequence 2, Appli	ω̈	Sequence 233, App	Sequence 8, Appli	Sequence 8, Appli	œ	10	10,		Sequence 2, Appli	4	ď	32,	65,	Sequence 65, Appl	Sequence 65, Appl
US-08-487-359-2	US-08-487-359-6	US-08-222-798A-2	US-08-222-798A-6	US-09-547-693-233	US-08-021-608D-8	US-08-726-160-8	PCT-US94-01782-8	US-08-021-608D-10	US-08-726-160-10	PCT-US94-01782-10	US-08-021-608D-2	US-08-726-160-2	PCT-US94-01782-2	US-08-642-255-32	US-07-609-716-65	US-08-475-411A-65	US-08-478-029A-65
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79	79	79	79	26	590	590	590	643	643	643	644	644	644	330	408	408	408
22.7	22.7	22.7	22.7	22.5	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	21.7	21.7	21.7	21.7
158	158	158	158	157	155	155	155	155	155	155	155	155	155	151.5	151.5	151.5	151.5
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## ALIGNMENTS

RESULT 1 US-09-976-594-64  i Sequence 64, Application US/09976594  i Patent No. 6673549  i GENERAL INFORMATION:  i APPLICANT: Buchbinder, Jenny  i TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  FILE REPERENCE: PA-0041 US  CURRENT APPLICATION NUMBER: US/09/976,594  CURRENT FILING DATE: 2001-10-12  i PRIOR PILING DATE: 2000-10-12	NUMBER OF SEQ ID NOS: 1143  SOFTWARE: PERL Program  SEQ ID NO 64  LENGTH: 525  TYPE: PRT  CRGANISM: Homo sapiens  FRATTRE:  NAME/KEY: misc_feature  NOTER INFORMATION: Incyte ID No. 6673549 085596CD1  US-09-976-594-64	Query Match Best Local Similarity 41.8%; Pred. No. 3.7e-21; Matches 64; Conservative 2; Mismatches 23; Indels 64; Gaps 8;	7 RPPPHGHIPHGPPPHGHPPHGHP-PHGPPP	Db 275 KPPFKPHGSRDHHHPHKPHEHGPPPPPDERDHSHGPPLPQGPPPLLPMSCSSCQH 329 Ov 41	330 ATFGINGAQRRSHNNNSSDLHPHKHSHEQHPHGHPHPHPHPHPHGH	Оу 68 РРНСИРРНОРРНОНРРНОНОРРВЯ 100	SULT 2 08-925-237-2 08-925-237-2 Sequence 2, Application US/08925237 PATENT No. 5981700 APPLICANT: Azen, Edwin A. APPLICANT: Pan, David APPLICANT: Pan, David TITLE OF INVENTION: Thereof Having Alpha-G
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US-08-925-237-4
Sequence 4, Application US/08925237
Patent No. 5881720
GENERAL INFORMATION:
APPLICANT: Azen, Edwin A.
APPLICANT: Pan, David
TITLE OF INVENTION: Thereof Having Alpha-Glucosidase Inhibitory Activity
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Kent Barta
STREET: 100 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 PPPEASPPESSPPDRQHPHPPRPNPPEASPPEPSPPNWQHPHPHPPRPNPEASPPEP 618
         -HPPHGPPPHGHPPHG
                                                                                                                                                                                              Squence 19, Application US/09281766

Patent No. 6376196

Patent No. 6376196

APPLICANT: Conrad, Patricia C.

APPLICANT: Touse, Kitland

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Recombinant Neospora Antigens and Their Uses

TITLE OF INVENTION: Recombinant Neospora Antigens and Their Uses

FILE REPRENCE: 023070-082510US

CURRENT APPLICATION NUMBER: US/09/281,766

CURRENT FILING DATE: 1999-03-30

PRIOR PILING DATE: 1999-03-30

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 19

LENGTH: 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             619 SPPNWOHPHPHPPRPNPPGASPPESSPPNWOHPHPHPRPNPP 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.8%; Score 208; DB 4;
37.9%; Pred. No. 1.8e-11;
tive 5; Mismatches 47
                                                  68 РРНGНРРНGРРРНGНРРНGНDНGPCDPP 98
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ATTORNEY/AGENT INFORMATION:
NAME: Barta, Kent S.
REGISTRATION NUMBER: 29,042
REFERENCE/DOCKET NUMBER: 96429/9002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Neospora sp.
CTHER INSORMATION: NC-p65 CDNA
US-09-281-766-19
                                                                                           daasadaasadaasada 69
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Best Local Similarity 37.9
Matches 39; Conservative
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ZIP: 53202-4108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                              US-09-281-766-19
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STATE:
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Patent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PPH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 PPQGGNQPQGPPPPPGKPQGPPPQGGNKPQGPPPGKPQGPPPQGDNKSQSARSPPGKPQ 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPPQGGNQPQGPPPPGKPQGPPPQG-----GNKSQGP--PPPGK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 GРРРН-GНРРНGРРНGНРРНGРРНGНРРНGНGГНDНGРCDPPSHK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 215.5; DB 4; Length 10
Pred. No. 5.7e-13;
0; Mismatches 41; Indels
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                                                                                                            STATE: n.a.
COUNTRY: USA
ZOUTE: 53202-4108
ZDIP: 53202-4108
ZDIP: 53202-4108
COMPUTER READABLE FORM:
REDING TYPE: ELOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BAR PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,237
FILING DATE:
CLASSIFICATION INFORMATION:
NAME: Barta, Kent S.
REGISTRATION NUMBER: 29,042
REFERENCE/DOCKET NUMBER: 96429/9002
TELEPOMUNICATION INFORMATION:
TELEPHONE: (608) 283-2275
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENERAL 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .7e-14;
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Pred. No. 3.7e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: OHU-04089
CURRENT PELLING NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 235
LENGTH: 104
                                           E: Kent Barta
100:East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.1%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial/Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
US-09-547-693-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kent Barts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-925-237-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                     Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-547-693-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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34.6%; Pred. No. 6.5e-09;
iive 4; Mismatches 41; Indels 42; Gaps
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JEACHOLO S. Application US/08217327

JEACHL INPORMATION:

APPLICANT: Barton, Maliyakal E
APPLICANT: Barton, Kenneth A

TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
NUMBER OF SEQUENCES: 16
CORRESPONDENCE MALIES and Brady
STREET: P.O. Box 2113
CITY: Madison
STREET: P.O. Box 2113
COUNTRY: USA
ZIP: 53701-2113
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PAPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
FILING DATE: 19-DEC-1991
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 27,386
STREET: Seay, MICHOLB STREET: PARCHAIN NUMBER: US/08/217,327
APPLICATION NUMBER: 27,386
STREET: Seay, MICHOLB STREET: PARCHAIN NUMBER: 19-DEC-1991
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 27,386
REGISTRATION NUMBER: 27,3
                                                                                                                                                                                                                                                                                                                                                                 Score 196; DB 2; Length 82;
Pred. No. 2.6e-11;
4; Mismatches 25; Indels
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                             TELEPHONE: (608) 257-3501
TELEPAX: (608) 283-2275
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
OUDECULE TYPE: protein
US-08-925-237-4
                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.1%;
Best Local Similarity 52.9%;
Matches 37; Conservative ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 34.64
Matches 46; Conservative
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61 VSTPPPTSSPPDVTASPPP----VSTPPPSSPPPATPPPASPPPATPPPASPPATPPPA 116
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US-US-11-32/-4
; Sequence 4, Application US/08217327
; Patent No. 5474925
; GENERAL INFORMATION:
APPLICANT: John, Maliyakal E
APPLICANT: John, Maliyakal E
APPLICANT: Barton, Remeth A
: TITLE OF INVENTYON: Immobilized Proteins in Cotton Fiber
NUMBER OF SEQUENCE: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STRRET: P.O. Box 2113
CITY: Madison
STRATE: W.
COUNTRY: USA
ZIP: 53701-2113
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/217,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.5%; Score 171; DB 1; Length 214; Best Local Similarity 44.0%; Pred. No. 1.1e-08; Matches 37; Conservative 1; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: SEAY, Nicholas
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 1122990831
TELECOMOUNICATION INFORMATION:
TELEPHONE: 608-251-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
mvrp: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 СИРРИСРРИСИРРИСИРР 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/07945283; Patent No. 5352596; GENERAL INFORMATION: APPLICANT: Cheung, Andrew K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-217-327-4
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39 РРРРЕНSРРРЕНSРРРРУНYESPPPKHSPPPTPVYKYKSPP--PMHSPPPYHFES

77.CO.CO E7 GDC TTJ

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65 нясьпрусняння в премення в пре
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 --GPPPHGHPPH---GPPPHGHPPH----GPPPHGHG-----PPHGHGFHDHGPGPPS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PPBNVPGPRFPDPNFPGPRFPDPNFPGPRFPDPNFPGPRFPDPNFPGPRF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 ЭнаанЭнаааЭнаанЭнаааЭна -анхаааЭнанЭнаааЭнаннЭнаааЭнаннЭнааа 8
                                                                                                                                                                                                                                                                                                              10 РИСИНРИ---СРРРИСИНРИ---СРРРИСИРРИ----СРРРКИРРИ--СРРРИСИРРИ-
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                        Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.1%; Score 161; DB 1; Length 79;
45.5%; Pred. No. 3.4e-08;
tive 4; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington, D.C.
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPUTER: PROPING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPHENINS-ANTIBIOTIC PEPTIDES
                                                                                                                                                                 Query Match 23.5%; Score 164; DB 3; Best Local Similarity 38.0%; Pred. No. 3.6e-08; Matches 46; Conservative 0; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W.
               FEATURE: OTHER INFORMATION: Histidine linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08487359 Patent No. 5633229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2000 FC....
CITY: Washington, D.C.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Matches 35; Conserva
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                                                                                      US-09-507-323B-13
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FACENT NO. 82/445.

APPLICANT: Choi, Jong Hyun
APPLICANT: Lee, Sang Yup
APPLICANT: Xu, Zhachui
TITLE OF INVENTION: EXPRESSION VECTORS COMPRISING A GENE
TITLE OF INVENTION: ENCODING OMPC DERIVED FROM E.COLI AS CELL SURFACE ANCHORING
TITLE OF INVENTION: MODITE: US/09/507,323B
TITLE OF INVENTION: WOTHER: US/09/507,323B
CURRENT APPLICATION NUMBER: RR 10-1999-0005773
FRIOR APPLICATION NUMBER: RR 10-1999-0005773
FRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 167
TYPE: PRT
ORGANISW: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 ЙОDPPGGGPPSAETHHHHQDPPGGGPPSTSSHHHHQDPPGGGPP-SPPRPSTSSSSSH 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.0%; Score 167; DB 1; Length 1958; 28.2%; Pred. No. 1.8e-07;
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
TITLE OF INVENTION: Involving The BPO and LLT Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSEE: Curtis P. Ribando
STREET: 1845 No. 5352596th University Street
                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: RIDBANG, CLURIS P
REGISTRATION NUMBER: 27976
TELEPHONE: 309-685-4011 ext.513
TELEPHON: 309-685-4011 ext.513
TELEPHON: 199-685-4128
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1958 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 48; Conserva
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                                                                                                                                                                                                                                                                   CITY: P
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-945-283-2
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Pred. No. 3.7e-08;
3; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/0822798A; Patent No. 5804553; Patent No. 5804553; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FORRSTER
STREET: 2000 Pennsylvania Ave. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY. USA
ZIP: 20006-1812
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR-1994
CLASSIFICATION: 514
CUUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUW TYPE: FIDEDPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCALIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995
CLASSITCATION: 514
PRIOR APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURABAIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 20,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPP---PPFRPPPFGPP 75
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TYPE: amino acids
STRANDEDNESS: single
JOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 46.8<sup>§</sup>
Matches 36; Conservative
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US-08-222-798A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
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Pred. No. 3.4e-08;
4; Mismatches 34; Indels
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Sequence 5, Application US/08487359

Patent No. 5633229

Patent No. 5633229

Patent No. 5633229

APPLICANT: KOKRYAKOV, VLADMIR N.

APPLICANT: HARMIG, SYLTA S.L.

APPLICANT: HARMIG, SYLTA S.L.

TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 РРРИСИРРИСРРИСИР 83
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Best Local Similarity 45.55
Matches 35; Conservative
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US-08-222-798A-3

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2000 Pennsylvania Ave. N.W.

Washington, D.

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63 ppp---pprrpppgpp 76

--PRHP 43

Gaps

51;

Sep 24 09:03:22 2004

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APPLICANT: VAN HERDE, GEORGE V.
APPLICANT: VAN HERDE, GEORGE V.
APPLICANT: VAN HERDE, GEORGE V.
APPLICANT: BOUWGTRA, JAN B.
APPLICANT: BOUWGTRA, JAN B.
APPLICANT: BOUNGTRA, JAN B.
APPLICANT: MCOBROEK, ANDREAS
APPLICANT: WERTEN, MAC.
APPLICANT: WERTEN, MAC.
APPLICANT: WENTEN, TRICHELE D.
APPLICANT: WIND, RIGHELE D.
APPLICANT: WENTEN, TRIVIA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION: BY SPEPARATION THEREOF
TITLE OF INVENTION: BY SPEPARATION THEREOF
TITLE OF INVENTION: SOUTHWER: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOUTHWARE: PALENTIN VEY: 2.1
SENGID NO 4
EBNGTH: 720
                                                                                                                                                                                                                                 63 PGAPGPAGPPGAPGPAGPPGAPGPPGAPGPAGPPGAPGPAGPPGAPGPAGPPGAPGP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 PGAPGPAGPPGAPPGPAGPPGPAGPAGPPGAPGPAGPPGAPGPPGAPGPPGAPGPPGAPGP 122
                                                                                                                              3 HGPAGPKGAHGPAGPKGAPGPAGPPGAPGPAGPPGAPGPAGPPGAPGPAGPPGAPGPAGP 62
                                                                                                                                                                                44 PHGPPPHGHP----PHGPP-----PHGPP------PHGPP------PHGHP-PHGPP-----P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 PHGPPPHGHP----PHGPP-----PHGHP-PHGPP-----PHGHP-PHGPP----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 HGPAGPKGAHGPAGPKGAPGPAGPPGAPGPAGPPGAPGPPGAPGPPGAPGPAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Illustrative OTHER INFORMATION: amino acid sequence
                                                                             6 НКР--РРИСИНРИСР------РРИСИНРИСРР------РИСИР-РИСРР-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 720;
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                           Indels
                           Mismatches 36;
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Pred. No. 2.8e-07;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- PPHGHHPHGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 HGHPPHGHG----FHDHGPCDP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09219849 Patent No. 6150081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 38.7%;
Matches 55; Conservative
                           55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 HRP--PPHGHHPHGP-
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                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                            23.0%; Score 160.5; DB 1; Length 78; 46.8%; Pred. No. 3.7e-08; tive 3; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence 49, Application US/08642255 | Patent No. 577349 |
| PATENT NO. 577349 |
| GENERAL INFORMATION: |
| APPLICANT: CAPPELLO, Joseph |
| APPLICANT: FERRARI, Franco A. |
| TITLE OF INVENTION: High Molecular Weight Collagen-Like |
| TITLE OF INVENTION: Protein Polymers |
| NUMBER OF SEQUENCES: 135 |
| NUMBER OF SEQUENCES: 135 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT |
| STREET: San Francisco |
| CITY: San Francisco |
| STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CALIFORNIA

ZIP: 94111-4187

ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
ATTONINY/ADATION H35
ATTONIANY/ADATION: A35
ATTONIANY/ADATION:
NAME: REFERENCE/POCKET NUMBER: 20,015
REFERENCE/POCKET NUMBER: 20,015
REFERENCE/POCKET NUMBER: A55556-3/BIR
TELEPAX: (415) 494-8770
TELEPAX: (415) 494-8770
TELEFAX: (415) 494-8771
TELEPAX: (415) 494-8771
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LEMETAX: 144 amino acida
                                                                       2000-0553.00
NAVE: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPK: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPP---PPFRPPPFGPP 75
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                                                                                                                                  linear
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US-08-222-798A-5
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US-08-642-255-49
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Gaps

51;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 23, 2004, 22:55:11; Search time 68.9558 Seconds (without alignments) 470.989 Million cell updates/sec Run on:

US-10-074-225A-6

697 1 SYNIIHRPPPHGHHPHGPPP......HPPHGHGFHDHGPCDPPSHK 101 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1349238 segs, 321558718 residues Searched:

1349238 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

The first of the f Published\_Applications\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

221499931, 22148680, 40, 20, 20, 20, 20, 20, 20, 20, 20, 20, 2	102, App
equence eq equence equence equence eq equence eq eq equence eq eq eq e	Sequence
US-10-424-599-221495 US-10-424-599-191976 US-10-424-599-191976 US-10-424-599-218680 US-10-424-599-224246 US-10-424-599-224246 US-10-424-599-224246 US-10-424-599-218681 US-10-424-599-218681 US-10-424-599-218181 US-10-424-599-218181 US-10-424-599-218182 US-10-424-599-21812 US-10-424-599-21812 US-10-424-599-163337 US-10-424-599-171754 US-10-424-599-171754 US-10-424-599-171754 US-10-424-599-171754 US-10-424-599-171754 US-10-424-599-171754 US-10-424-599-171754 US-10-424-599-171754 US-10-424-599-171754 US-10-424-599-1718067 US-10-424-599-1718067 US-10-424-599-1718067 US-10-424-599-1718067 US-10-424-599-1718067 US-10-424-599-1718067 US-10-424-599-171818067 US-10-424-599-171818067 US-10-424-599-171818067 US-10-424-599-171818067 US-10-424-599-171818067 US-10-424-599-171818067 US-10-437-963-11818187	-10-403
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## ALIGNMENTS

US-10-074-225A-6

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Sequence 6, Application US/10074225A
; Sequence 6, Application US/10074225A
; Bublication No. US20030082740A1
; GENERAL INFORMATION:
; APPLICANT: PLUNKETT, Marian L
; APPLICANT: PLUNKETT, Marian L
; APPLICANT: HARRIS, Scott
; APPLICANT: HARRIS, Scott
; TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC
; TITLE OF INVENTION: ANTI-THOM AGENT
; FILE REFERENCE: 38442-178463
; CURRENT APPLICATION NUMBER: US/10/074,225A
; CURRENT APPLICATION NUMBER: US 60/268,370
; PRIOR FILING DATE: 2001-02-14
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Version 3.1
; TEMPLO APPLICATION NUMBER: US/10/074,225A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GHPPHGPPPHGHPPHGHPHGHPHGHGFHDHGPCDPPSHK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 697; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
COGANISM: Lepus americanus
US-10-074-225A-6
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RESULT 2

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
PLUNKETT, Marian L
APPLICANT:
APPLICANT:
MAZAR, Andrew P

TITLE OF INVENTION:
HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC
TITLE OF INVENTION:
FILE REPERRNCE:
SA342-17463
CURRENT FILING DATE:
2002-02-14
PRIOR APPLICATION NUMBER: US 60/268,370
PRIOR APPLICATION NUMBER: US 60/268,370
PRIOR PILING DATE:
SOUTHWARE:
PRIOR PILING DATE:
SOUTHWARE:
SOUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DONATE, Fernando
APPLICANT: DINKETT, Marian L
APPLICANT: PLUNKETT, Marian L
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC
TITLE OF INVENTION: ANTI-TUMOR AGENT
FILE OF INVENTION: ANTI-TUMOR AGENT
FILE REPERENCE: 38342-178463
CURRENT FILING DATE: 2002-02-14
PRIOR PILING DATE: 2001-02-14
RICH REPLICATION NUMBER: US 60/268,370
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 314; DB 14; Length 525;
Pred. No. 5.9e-15;
2; Mismatches 23; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 КРР--РИG----НИРИСРРИСНИРИСРР------НGНР-РИСРРР
390 НРНСНИРНСНИРНСНИРНСКОРСОРРРН 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 PPHGHPPHGPPPHGHPPHGHGFCDPPSH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-074-225A-1; Sequence 1, Application US/10074225A; Publication No. US20030082740A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10074225A Publication No. US20030082740A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.8%;
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 47; Conservat
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US-10-074-225A-5
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   Sequence 3, Application US/10074225A
Publication No. US20030082740A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PLUNKETT, Marian L
APPLICANT: PLUNKETT, Marian L
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: ANTI-TUMOR AGENT
TITLE OF INVENTION: ANTI-TUMOR AGENT
FILE REFRENCE: 38342-178463
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT FILING DATE: 2002-02-14
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
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Publication No. US20030108871A1
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REPERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 62
LENGTH: 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 RPP--PHG----HHPHGPPHGHHPHGPPP-----HGHP-PHGPP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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OTHER INFORWATION: Incyte ID No. US20030108871A1 085596CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 СИРРИСРРИСИРРИСРРИСИРРИСИРИСИСЕН 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHPPHGPPPHGHPPHGHPPHGHPFHDHGPCDPPSHK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 697; DB 14;
Pred. No. 5.6e-42;
0; Mismatches 0;
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41.8%; Pred. No. 5.9e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 526
TYPE: PRT
CRGANISM: Lepus americanus
US-10-074-225A-3
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Best Local Similarity 100.
Matches 101, Conservative
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Best Local Similarity 41.8
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 223180, Application US/10424599
; Sequence 223180, Application US/10424599
; Publication No. US20040031072A1
GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: Cao Yongwei
    APPLICANT: Cao Yongwei
    APPLICANT: APPLICANT: APPLICANT: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILLE REFREENCE: 38-21(3523)B
    CURRENT APPLICATION NUMBER: US/10/424,599
    CURRENT FILING DATE: 2003-04-28
    NUMBER OF SEQ ID NOS: 285684
    SEQ ID NO 223180
    LENGTH: 241
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33.5%; Score 233.5; DB 12; Length 241;
Best Local Similarity 48.0%; Pred. No. 1.6e-09;
Matches 49; Conservative 3; Mismatches 39; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
35.3%; Score 246; DB 9; Length 274;
Best Local Similarity 47.1%; Pred. No. 2.3e-10;
Matches 57; Conservative 1; Mismatches 29; Indels 3
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,887
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                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/087,678
FILING DATE: «UNKNOWN PILING DATE: «UNKNOWN NAME: CERRONE, MICHAEL C. REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 99,132
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: 9206712
SEQUENCE DESCRIPTION: SEQ ID NO: 4
                                                                                                                                FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CRARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
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ORGANISM: Glycine max
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US-10-424-599-223180
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FULE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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        30; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 --HGHPPHGPPPHGHPPHGPPPHGH----PPHGHGFH-----DHGPCDPPSH 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gorgone, Gina
TITLE OF INVENTION: THYROID AND PITUITARY MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_69430C.1.pep
US-10-437-963-171176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEB: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(235)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                70 НСИРРИСРРИСИРРИСИСКИПРЕН 100
                                                                                                                                                                                   43 HGHHPHGHHPHGHPHCHDFQDYGPCDPPPH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 171176, Application US/10437963;
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Qao, Yongwei
APPLICANT: Wu, Wai
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbaguk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09850887
Patent No. USZ0020009778A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 171176
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-850-887-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 КРРРИСИНРИСРРИСИНРИСРРИСИРРИСРРИСЬ РРИ-СРРИСИРРИ-СРРИСИРИ-СРРИСИР 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 233.5; DB 16; Length 309;
Pred. No. 1.9e-09;
3; Mismatches 39; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 233.5; DB 16; Length
Pred. No. 1.9e-09;
3; Mismatches 39; Indels
                                       64 РН-СРРРНСНРРН-СРРРНСНРРНСНСРС-- ПРРЅНК 101
                                                                    151 РИБКРРРЕУОРРИЕКРРРЕУОРРИККРРРЕНОРРИВКРРЕНО 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 РН-СРРРИСИРРН-СРРРИСИРРИСИСТИПИСРС-- ОРРЅНК 101
                                                                                                                                                                                                                              APPLICANT: Fransen, Henk J
APPLICANT: Bisseling, Anton H
TITLE OF INVENTION: ENDOS Gene Regulatory Region
TITLE APPLICATION OF STEDS
CURRENT APPLICATION NUMBER: US/10/751,014
CURRENT APPLICATION NUMBER: US/09/564,142A
PRIOR APPLICATION NUMBER: US/09/564,142A
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 6
SOFTHARE: Patentin version 3:1
SEQ ID NO.
LUNGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10751014
| Publication No. US20040172676A1
| GENERAL INFORMATION:
| APPLICANT: Bisseling, Anton H
| TITLE OF INVENTION: BNOD2 Gene Regulatory Region
| FILE REFRENCE: MPS 4-87FD2
| CURRENT APPLICATION NUMBER: US/10/751,014
| CURRENT FILING DATE: 2000-05-03
| PRIOR FILING DATE: 2000-05-03
| PRIOR FILING DATE: 1997-05-20
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: PATENTIN VENTION 3.1
                                                                                                                                                                            ; Sequence 2, Application US/10751014; Publication No. US20040172676A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 48.0%;
Matches 49; Conservative
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Best Local Similarity 48.0°
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                      RESULT 9
US-10-751-014-2
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KPPPBYQPPHEKPPH----ENPPPEHGPPHEKPPHEKPPPEXTPPHEKPPFSYQP 150

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7 КРРРИСИНРИСРРИСИНРИСРРИСИРРИСРРИСИ-РРИ-СРРИСИРРИ-СРРИСИРИ-СРРИСИР

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US-10-424-599-281824

US-10-424-599-281824

Sequence 281824, Application US/10424599

Publication No US20040031072A1

FOBERAL INFORMATION:

APPLICANT: EA ROSA Thomas J

APPLICANT: EXOU Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Janats and Uses Thereof for Plant Improvement

TITLE OF SET INVENTION: 19-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ENGITH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 НІНРНРНРЕРРРККРУХУНБРРРРИНРНРУРН-РНРНРЧРНРЧРНРНРНРНРНРНР 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 H-GPPPHGHPP-----HGPPP--HGHP-PHGPPPHGHP-PHGHGP-HDHGP----C 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 РРРИСНИРИСРРРИСИ-НРИСРРРИСИРР---НСРРРИСИРР-----НСРР---НСРР--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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APPLICANT: Tably, Bing
APPLICANT: Table, Bing
APPLICANT: Gland, Bradford W.
APPLICANT: Gland, Bradford W.
APPLICANT: Gland, Cary M.
APPLICANT: Gland, Cary M.
APPLICANT: Gland, Cary M.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DEBNITED IN THE MITOCHONDRIAL PROFEOME
TITLE OF INVENTION NUMBER: US/10/408,765A
CURRENT APPLICANTON NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 232.5; DB 12; Length 342;
Pred. No. 2.4e-09;
1; Mismatches 25; Indels 39;
64 РН-GРРРИGНРРН-GРРРНGНРРНGНGFHDHGPC--DPPSHK 101
                                             151 РНЕКРРРЕУОРРНЕКРРЕУОРРНЕКРРЕНОРРНЕКРРЕНО 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | FEATURE:
| OTHER INFORMATION: Clone ID: PAT_MRT3847_96507C.1.pep
US-10-424-599-281824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(342)
OTHER INFORMATION: unsure at all Xaa locations
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22-10-402-65A-69
; Sequence 69, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Fahy, Foin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 33.4%;
1 Similarity 48.4%;
61; Conservative 1
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ORGANISM: Glycine max
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 61, Conserva
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Query Match
Best Local Similarity 48.2%
Matches 54; Conservative
SOFTWARE: Patentin Ver. 2.0
                                                                                          ; ORGANISM: Homo sapiens
US-09-997-003-44
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ORGANISM: Glycine max
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US-10-424-599-234553
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                       SEQ ID NO 44
LENGIH; 93
                                                                        TYPE: PRT
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Best Local
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                                                                                                                                                                                                                                                                                   93 ОСРРРРРЕКРОСРРРОССИКРОСРРРС-КРОСРРРОСТИКОСРРРОСТИКОСРРРОС-СИ 150
                                                                                                                                           33 PPPPPGKPQGPPPQGGNKPQGPPPPGKPQGPPPQGGKRSRSPRSPRSPPGKPQGPPPQGGNQP 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 PPPHGH------HPHG----PPPHGHHPHGPPPHGHP-PHGPPPRHPPH--GPPP-HGH 52
                                                                                                                                                                                                                                       45 HGPPPHGHPPHGPPH-GHPPHGPPHGHPPHGPPHGH------PPHGHGF 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/09997003

Publication No. US20030203361A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/997,003

CURRENT APPLICATION NUMBER: unassigned

PRIOR PEPLING DATE: 2001-11-30

PRIOR PEPLING DATE: 2001-11-30

PRIOR PELING DATE: 2001-08-11

PRIOR PELING DATE: 2001-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.8%; Score 228.5; DB 11; Length 93; 54.7%; Pred. No. 1.7e-09; ive 0; Mismatches 20; Indels 23
                                           33.1%; Score 231; DB 16; Length 173; 40.3%; Pred. No. 1.9e-09; tive 4; Mismatches 33; Indels 4C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA003P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 ЭНСЕБРИСИВРИСТЕРНИСТЕР-ИСТЕРНИСТВИ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 СРССРРИ----НСРСРССРРЕНСР---СИРРРС 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/997,003
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: unsesigned
PRIOR PILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: PCT/US00/22157
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/148,680
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-997-003-44; Application US/09997003; Sequence 44, Application US/09997013; Publication NO US20030203361A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 93
                                      0uery Match
Best Local Similarity 40.34
Matches 52, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  151 QPQGPPPPP 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
US-10-408-765A-69
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GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Xovalic David K

APPLICANT: Xovalic David K

APPLICANT: Ano Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21 (53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 234553
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                                                                                                                               8 PPPHCH-----HPHG----PPPHGHPHGHPHCHP-PPHGHP-PPPH--GPPP-HGH 52
                                                                                                                                                                                           3 PGPKGHCHCGGHGHPPGHCGPPPGHGPGPCGPPPHHGPGPCGPPHHGPGPCGPPPGHGP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.6%; Score 227.5; DB 12; Length 107;
48.2%; Pred. No. 2.3e-09;
tive 3; Mismatches 28; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ІНКРРИС----РИСРРИСН---НРИСРРИСН----РКНРРИСР----РКНРРИС
                                                                   Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 НР-- СРРЕРСЯНОННСРРСРРУАНРТРРРСРРСРР----- РСРРХРРТ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 НРРИСРРИС-НРРИСР - РРИСИРРИСР - РИСИРРИСИСИОРИЗ 99
   DB 11; Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53829C.1.pep US-10-424-599-234553
                                                                   20;
                                                                                                                                                                                                                                                                 53 РРНСРРИЧИРРНСРРИЧИРР-НСРРИЧИРВ 86
                                                                                                                                                                                                                                                                                                                          63 GPCGPPH----HGPGPCGPPPGHGP---GHPPPG 90
ch 32.8%; Score 228.5; DB 1
| Similarity 54.7%; Pred. No. 1.7e-09;
52; Conservative 0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(107)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: September 23, 2004, 23:11:17 Job time : 69.9558 secs
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